IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:
HANNA *et al.*
Appl. No. 09/030,832
Filed: February 26, 1998
For: **$GABA_A$ Receptor Epsilon Subunits**



Art Unit: 1646
Examiner: Landsman, R.
Atty. Docket: 1488.0950001/EKS/KKV

#17
KO
10-11-00

# Declaration of Ewen F. Kirkness and Michael C. Hanna Under 37 C.F.R. § 1.131

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

We, Ewen F. Kirkness and Michael C. Hanna hereby declare and state as follows:

1. We are named inventors of the captioned application. This declaration is made to establish completion of the claimed invention in the United States at a date prior to March 8, 1997, the earliest effective date of Garret *et al.*, *J. Neurochem. 68*:1382-1389 (1997) (hereinafter "Garret *et al.*").

2. As much of the claimed invention that is disclosed in Garret *et al.* was completed in this country before March 8, 1997. The following is provided as evidence to such completion. Before March 8, 1997, we identified a human DNA sequence which we understood to encode a novel $GABA_A$ receptor subunit, which we designated as the epsilon subunit. Exhibit A consists of a copy of a notebook page which provides the basis for the foregoing demonstration. The date which has been redacted from Exhibit A is prior to March 8, 1997.

Also before March 8, 1997, we possessed a nucleotide sequence having the designation GRE #5.seq, with a coding region identical to the coding region from nucleotides 41 to 1561 in SEQ ID NO:41 of the captioned application, and which encodes amino acids -18 to 488 in SEQ ID NO:42 of the captioned application. Exhibit B consists of a copy of a notebook page disclosing the nucleotide sequence which provides the basis for the foregoing demonstration. The date which has been redacted from Exhibit B is prior to March 8, 1997.

3. As the persons signing below:

We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patents issued thereupon.

09/25/00
Date

Ewen F. Kirkness

Date

Michael C. Hanna

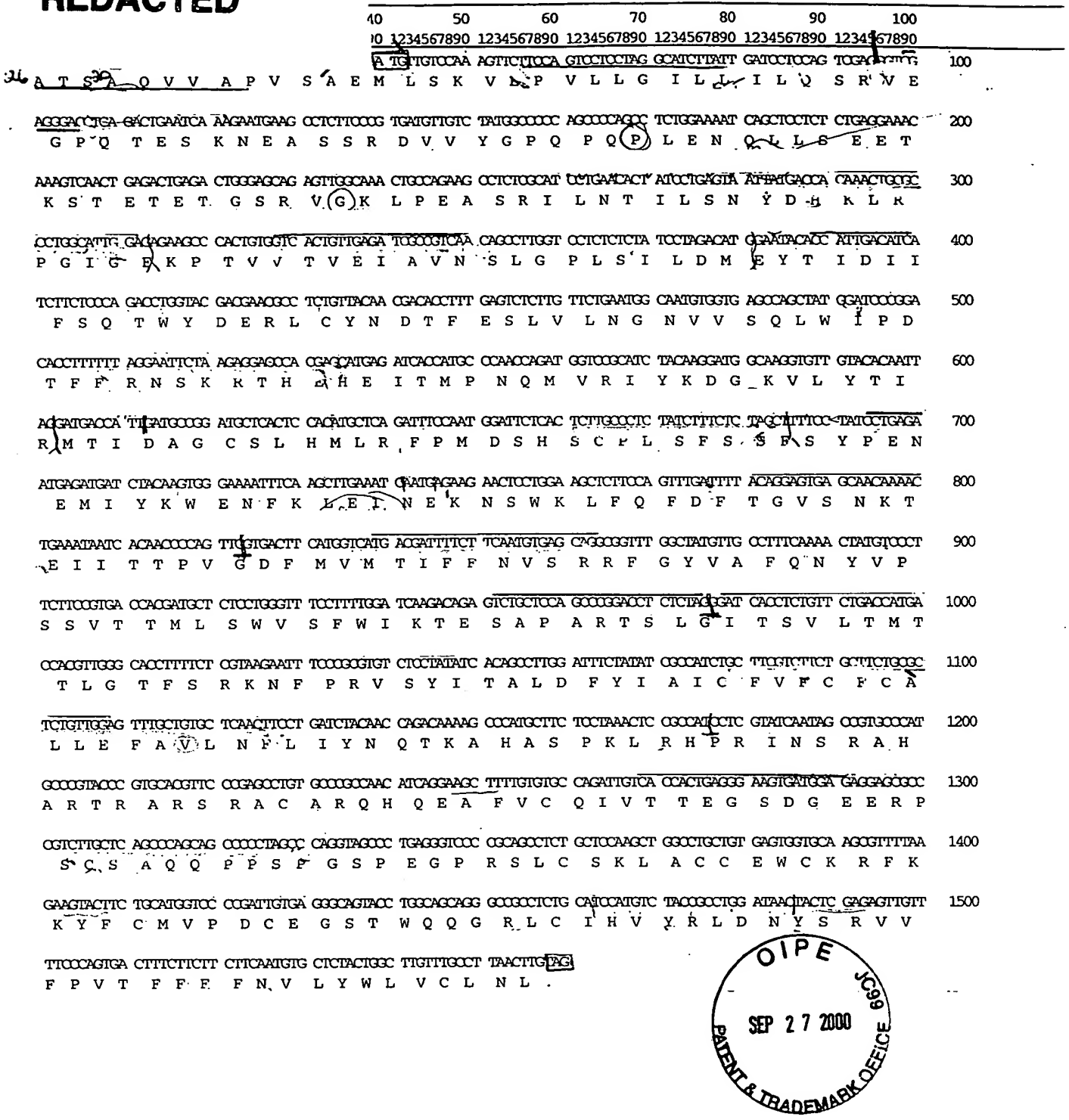
A tblastn search of GenBank (release 89) with GRP.pep hit a human EST sequence that appears to encode a novel GABA-A receptor subunit.

The novel subunit is christened the first epsilon subunit (GRE).

Exhibit B
09/030,832

GRE#5.seq Sequence

**REDACTED**



Due Date: None

Applicants: Hanna *et al.*

Art Unit: 1801

Examiner: to be assigned

Application No.: 09/030,832

Docket: 1488.0950001

Filed: February 26, 1998

Atty: EKS/SGW

For: **$GABA_A$ Receptor Epsilon Subunits**

When receipt stamp is placed hereon, the USPTO acknowledges receipt of the following documents:

1. Transmittal letter (in duplicate); 2. Information Disclosure Statement; 3. Form PTO-1449 (20 pages); and 4. Copies of references AL1, AR1, AS1, AT1, AR2, AS2, AT2, AR3, AS3, AT3, AR4, AS4, AT4, AR5, AS5, AT5, AR6, AS6, AT6, AR7, AS7, AT7, AR8, AS8, AT8, AR9, AS9, AT9, AR10, AS10, AT10, AR11, AS11, AT11, AR12, AS12, AT12, AR13, AS13, AT13, AR14, AS14, AT14, AR15, AS15, AT15, AR16, AS16, AT16, AR17, AS17, AT17, AR18, AS18, AT18, AR19, AS19, AT19, AR20, and AS20.

**Please Date Stamp And Return To Our Courier**


NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = R07883 | |
|---|---|
| *gi* | *Update Date* |
| 159806 | 04/06/95 |

***This sequence was released by NCBI on 04/06/95***

Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez2 ?

Other Formats: FASTA Graphic

```
LOCUS       R07883         317 bp    mRNA            EST       05-APR-1995
DEFINITION  yf16g04.s1 Homo sapiens cDNA clone 127062 3' similar to
            SP:GAC4_CHICK P34904 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4
            SUBUNIT PRECURSOR ;.
ACCESSION   R07883
NID         g759806
KEYWORDS    EST.
SOURCE      human clone=127062 library=Soares fetal liver spleen 1NFLS
            vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
            (ampicillin resistant) primer=-21m13 Rsite1=Pac I Rsite2=Eco RI
            Liver and spleen from a 20 week-post conception male fetus. 1st
            strand cDNA was primed with a Pac I - oligo(dT) primer [5'
            AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
            I and cloned into the Pac I and Eco RI sites of the modified pT7T3
            vector.  Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 317)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 241
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..317
                     /organism="Homo sapiens"
                     /clone="127062"
BASE COUNT       98 a      64 c      91 g      57 t       7 others
ORIGIN
        1 ntgtctggtt gtagatcagg aagttgagca cagcaaactc caacagagcg cagaagcaga
       61 agacgaagca gatggcgata tagaaatcca aggctgtgat ataggagaca cgcgggaaat
      121 tcttacgaga aaaggtnccc aacgtggtca tggtcagaac agaggtgatc cctagagagg
      181 tccgggctgg agcagactct gtcttgatcc naaaaggaaa cccagggaga gcatcgtggg
      241 tcacggaaga ngggacatag ttttgaaagg caccatagcc aaanccgcct nctcacattt
      301 gaggaanttc gtcattg
//
```

Save the above report in Macintosh [ ] Text [ ] format.

>gb|R07883|R07883 yf16g04.s1 Homo sapiens cDNA clone 127062 3' similar to SP:GAC4_CHICK P34904 GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-4 SUBUNIT PRECURSOR ;.
Length = 317

Minus Strand HSPs:

Score = 622 (171.9 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 130/138 (94%), Positives = 130/138 (94%), Strand = Minus / Plus

```
Query:  4096 GGCTGTGATATAGGAGACACGCGGGAAATTCTTACGAGAAAAGGTGCCCAACGTGGTCAT 4037
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct:    92 GGCTGTGATATAGGAGACACGCGGGAAATTCTTACGAGAAAAGGTNCCCAACGTGGTCAT 151

Query:  4036 GGTCAGAACAGAGGTGATCCCTAGAGAGGTCCGGGCTGGAGCAGACTCTGTCTTGATCCA 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   152 GGTCAGAACAGAGGTGATCCCTAGAGAGGTCCGGGCTGGAGCAGACTCTGTCTTGATCCN 211

Query:  3976 AAAGGAAACCCAGGAGAG 3959
              ||| | || ||  | |||
Sbjct:   212 AAAAGGAAACCCAGGGAG 229
```

Score = 212 (58.6 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 44/47 (93%), Positives = 44/47 (93%), Strand = Minus / Plus

```
Query:  3952 GGTCACGGAAGAAGGGACATAGTTTTGAAAGGCAACATAGCCAAACC 3906
             |||||||||||| |||||||||||||||||||| |||||||||| |
Sbjct:   239 GGTCACGGAAGANGGGACATAGTTTTGAAAGGCACCATAGCCAAANC 285
```

Score = 90 (24.9 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 22/27 (81%), Positives = 22/27 (81%), Strand = Minus / Plus

```
Query:  3977 AAAAGGAAACCCAGGAGAGCATCGTGG 3951
             ||| | || ||  ||||||||||||||
Sbjct:   213 AAAGGAAACCCAGGGAGAGCATCGTGG 239
```

Score = 88 (24.3 bits), Expect = 5.1e-63, Sum P(4) = 5.1e-63
Identities = 22/29 (75%), Positives = 22/29 (75%), Strand = Minus / Plus

```
Query:  3912 CCAAACCGCCTGCTCACATTGAAGAAAAT 3884
             | || |||||| ||||||||  || || |
Sbjct:   280 CAAANCCGCCTNCTCACATTTGAGGAANT 308
```

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = R07942 | |
|---|---|
| ***gi*** | ***Update Date*** |
| 159862 | 04/06/95 |

***This sequence was released by NCBI on 04/06/95***

Direct Link

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

```
LOCUS       R07942         477 bp    mRNA            EST       05-APR-1995
DEFINITION  yf16g04.r1 Homo sapiens cDNA clone 127062 5'.
ACCESSION   R07942
NID         g759865
KEYWORDS    EST.
SOURCE      human clone=127062 library=Soares fetal liver spleen 1NFLS
            vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
            (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI
            Liver and spleen from a 20 week-post conception male fetus. 1st
            strand cDNA was primed with a Pac I - oligo(dT) primer [5'
            AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
            I and cloned into the Pac I and Eco RI sites of the modified pT7T3
            vector.  Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 323
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..477
                     /organism="Homo sapiens"
                     /clone="127062"
BASE COUNT       92 a    103 c    123 g    151 t      8 others
ORIGIN
        1 tgtaggacag tgaactgaga aggaagctat taagattctg gccttggtta gctctcaact
       61 ggccattggt cttgcagtaa gtctttttc tgggcttctt ctggtcctat ttgtatgtat
      121 tgcattgtca catcatgcct ctatcctagg gaatactgtg agctgaaaaa tgagaccctt
      181 actgttcacg tcctgctaag ggggaccgtc gtgtcagcac tgtaatgcag tgatgttttt
      241 tgtgtctttc aggtgacttc atgggtcatg acgattttct tcaatgtgag cagggcggtt
      301 tgggctatgt tgcctttcaa aactatgtcc ccttcttccc gtgaccacgg atggtctccn
      361 ggggtttccn ttttggancc aagacaggag tctggntcca gccccgggac ctttttaggg
      421 gatcaacnct cgttncggac catggaccac gttgggggna acttttnttc gtaagga
//
```

Save the above report in Macintosh Text format.

>gb|R07942|R07942 yf16g04.r1 Homo sapiens cDNA clone 127062 5'.
Length = 477

Plus Strand HSPs:

Score = 1089 (300.9 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 221/225 (98%), Positives = 221/225 (98%), Strand = Plus / Plus

```
Query:  3651 GCCTTGGCTTAGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCT 3710
             | | | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    40 GGCCTTGGTTAGCTCTCAACTGGCCATTGGTCTTGCAGTAAGTCTTTTTTCTGGGCTTCT 99

Query:  3711 TCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGT 3770
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   100 TCTGGTCCTATTTGTATGTATTGCATTGTCACATCATGCCTCTATCCTAGGGAATACTGT 159

Query:  3771 GAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCA 3830
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   160 GAGCTGAAAAATGAGACCCTTACTGTTCACGTCCTGCTAAGGGGGACCGTCGTGTCAGCA 219

Query:  3831 CTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGG 3875
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   220 CTGTAATGCAGTGATGTTTTTTGTGTCTTTCAGGTGACTTCATGG 264
```

Score = 236 (65.2 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 48/49 (97%), Positives = 48/49 (97%), Strand = Plus / Plus

```
Query:  3611 TGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGCT 3659
             ||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct:     1 TGTAGGACAGTGAACTGAGAAGGAAGCTATTAAGATTCTGGCCTTGGTT 49
```

Score = 159 (43.9 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 35/39 (89%), Positives = 35/39 (89%), Strand = Plus / Plus

```
Query:  3874 GGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGG 3912
             |||||||||||||||||||||||||||||  | || |
Sbjct:   264 GGTCATGACGATTTTCTTCAATGTGAGCAGGGCGGTTTG 302
```

Score = 153 (42.3 bits), Expect = 1.3e-114, Sum P(4) = 1.3e-114
Identities = 33/36 (91%), Positives = 33/36 (91%), Strand = Plus / Plus

```
Query:  3906 GGTTTGGCTATGTTGCCTTTCAAAACTATGTCCCTT 3941
             | || |||||||||||||||||||||||||||| |
Sbjct:   298 GTTTGGGCTATGTTGCCTTTCAAAACTATGTCCCCT 333
```

Doc. Ref. AS17
Appl. No. 09/030,832



NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = C17228 | |
|---|---|
| ***gi*** | ***Update Date*** |
| 1571935 | 06/02/97 |

***This sequence was released by NCBI on 09/29/96***
Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

```
LOCUS       C17228         293 bp    mRNA            EST       04-SEP-1996
DEFINITION  Human placenta cDNA 5'-end GEN-542A05.
ACCESSION   C17228
NID         g1571935
KEYWORDS    EST; EST(expressed sequence tag); Human placenta.
SOURCE      Homo sapiens placenta cDNA to mRNA, clone:542A05.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE   1  (sites)
  AUTHORS   Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
            Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
            Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
            Maekawa,H., Nakamura,Y. and Takahashi,E.
  TITLE     Otsuka cDNA project
  JOURNAL   Unpublished (1996)
REFERENCE   2  (bases 1 to 293)
  AUTHORS   Fujiwara,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
            Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
            Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
            Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES             Location/Qualifiers
     source          1..293
                     /organism="Homo sapiens"
                     /clone="542A05"
                     /tissue_type="placenta"
BASE COUNT       74 a      68 c      81 g      70 t
ORIGIN
        1 gtgaaacagg gagccaccaa aactttgggg agcaggctag tgccggtttt gaccacctgt
       61 ggagcagtgc tcactcacga aggcattttg ccatcacatg aatgtgcaga aaggaggcca
      121 aaagcattct gtgcttctcc accacagcac agacttccct agtctcattt gctgagagta
      181 gacattctga gggccagcag tgcaggtgtg atgtgcctca gagggtatga gcccttagtc
      241 agccatctgg atatcagctg cgtgggcatg atatctagaa ggctaattga ttt
//
```

Save the above report in Macintosh Text format.

>gb|C17228|C17228 Human placenta cDNA 5'-end GEN-542A05.
Length = 293

Plus Strand HSPs:

Score = 1153 (318.6 bits), Expect = 6.3e-109, Sum P(2) = 6.3e-109
Identities = 233/236 (98%), Positives = 233/236 (98%), Strand = Plus / Plus

```
Query:  3268 GTGAAACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGT 3327
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     1 GTGAAACAGGGAGCCACCAAAACTTTGGGGAGCAGGCTAGTGCCGGTTTTGACCACCTGT 60

Query:  3328 GGAGCAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCA 3387
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    61 GGAGCAGTGCTCACTCACGAAGGCATTTTGCCATCACATGAATGTGCAGAAAGGAGGCCA 120

Query:  3388 AAAGCATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTA 3447
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   121 AAAGCATTCTGTGCTTCTCCACCACAGCACAGACTTCCCTAGTCTCATTTGCTGAGAGTA 180

Query:  3448 GACATTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAAGCCCT 3503
             ||||||||||||||||||||||||||||||||||||||||||||||||||  || |
Sbjct:   181 GACATTCTGAGGGCCAGCAGTGCAGGTGTGATGTGCCTCAGAGGGTATGAGCCCTT 236
```

Score = 320 (88.4 bits), Expect = 6.3e-109, Sum P(2) = 6.3e-109
Identities = 64/64 (100%), Positives = 64/64 (100%), Strand = Plus / Plus

```
Query:  3498 AGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTG 3557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   230 AGCCCTTAGTCAGCCATCTGGATATCAGCTGCGTGGGCATGATATCTAGAAGGCTAATTG 289

Query:  3558 ATTT 3561
             ||||
Sbjct:   290 ATTT 293
```

Doc. Ref. AT17
Appl. No. 09/030,832



NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = Y07637 | |
|---|---|
| *gi* | *Update Date* |
| 174370 | 03/05/97 |

***This sequence was released by NCBI on 12/20/96***

Dist... INT

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

Links: MEDLINE Protein Related Sequences

```
LOCUS       HSGABACHL    3153 bp    RNA             PRI       03-MAR-1997
DEFINITION  H.sapiens mRNA for putative GABA-gated chloride channel.
ACCESSION   Y07637
NID         g1747370
KEYWORDS    GABA-gated chloride channel.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3153)
  AUTHORS   Garret,M., Bascles,L., Boue-Grabot,E., Sartor,P., Charron,G.,
            Bloch,B. and Margolskee,R.F.
  TITLE     An mRNA encoding a putative GABA-gated chloride channel is
            expressed in the human cardiac conduction system
  JOURNAL   J. Neurochem. 68, 1382-1389 (1997)
REFERENCE   2  (bases 1 to 3153)
  AUTHORS   Garret,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-1996) M. Garret, CNRS UMR5543, Laboratoire de
            Neurophysiologie, Universite de Bordeaux2, 146 rue Leo Saignat,
            33076 Bordeaux Cedex, FRANCE
FEATURES             Location/Qualifiers
     source          1..3153
                     /organism="Homo sapiens"
     CDS             51..1568
                     /function="expressed in cardiac conduction system"
                     /codon_start=1
                     /product="putative GABA-gated chloride channel"
                     /db_xref="PID:e274573"
                     /db_xref="PID:g1747371"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPGDFMVMTIFFNVSRRF
                     GYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRVS
                     YITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRAR
                     SRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWCK
                     RFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     polyA_signal    3118..3123
BASE COUNT      726 a    885 c    687 g    855 t
ORIGIN
        1 agagcgtgag cgcgacctcc gcgcaggtgg tggcgccggt ctccgcggaa atgttgtcca
       61 aagttcttcc agtcctccta ggcatcttat tgatcctcca gtcgagggtc gagggacctc
      121 agactgaatc aaagaatgaa gcctcttccc gtgatgttgt ctatggcccc cagccccagc
      181 ctctggaaaa tcagctcctc tctgaggaaa caaagtcaac tgagactgag actgggagca
      241 gagttggcaa actgccagaa gcctctcgca tcctgaacac tatcctgagt aattatgacc
      301 acaaactgcg ccctggcatt ggagagaagc ccactgtggt cactgttgag atcgccgtca
      361 acagccttgg tcctctctct atcctagaca tggaatacac cattgacatc atcttctccc
      421 agacctggta cgacgaacgc ctctgttaca acgacacctt tgagtctctt gttctgaatg
      481 gcaatgtggt gagccagcta tggatcccgg acacctttt taggaattct aagaggaccc
      541 acgagcatga gatcaccatg cccaaccaga tggtccgcat ctacaaggat ggcaaggtgt
      601 tgtacacaat taggatgacc attgatgccg gatgctcact ccacatgctc agatttccaa
      661 tggattctca ctcttgccct ctatctttct ctagctttc ctatcctgag aatgagatga
      721 tctacaagtg ggaaaatttc aagcttgaaa tcaatgagaa gaactcctgg aagctcttcc
      781 agtttgattt tacaggagtg agcaacaaaa ctgaaataat cacaacccca ggtgacttca
      841 tggtcatgac gattttcttc aatgtgagca ggcggtttgg ctatgttgcc tttcaaaact
      901 atgtcccttc ttccgtgacc acgatgctct cctgggtttc cttttggatc aagacagagt
      961 ctgctccagc ccggacctct ctagggatca cctctgttct gaccatgacc acgttgggca
     1021 ccttttctcg taagaatttc ccgcgtgtct cctatatcac agccttggat ttctatatcg
     1081 ccatctgctt cgtcttctgc ttctgcgctc tgttggagtt tgctgtgctc aacttcctga
     1141 tctacaacca gacaaaagcc catgcttctc ctaaactccg ccatcctcgt atcaatagcc
     1201 gtgcccatgc ccgtacccgt gcacgttccc gagcctgtgc ccgccaacat caggaagctt
     1261 ttgtgtgcca gattgtcacc actgagggaa gtgatggaga ggagcgcccg tcttgctcag
     1321 cccagcagcc ccctagccca ggtagccctg agggtccccg cagcctctgc tccaagctgg
     1381 cctgctgtga gtggtgcaag cgttttaaga agtacttctg catggtcccc gattgtgagg
     1441 gcagtacctg gcagcagggc cgcctctgca tccatgtcta ccgcctggat aactactcga
```

```
      1501 gagttgtttt cccagtgact ttcttcttct tcaatgtgct ctactggctt gtttgcctta
      1561 acttgtaggt accagctggt accctgtggg gcaacctctc cagttccccc aggaggtcca
      1621 agccccttgc caagggagtt gggggaaagc agcagcagca gcaggagcga ctagagtttt
      1681 tcctgcccca ttccccaaac agaagcttgc agagggtttg tctttgctgc ccctctcccc
      1741 tacctggccc attcactgag tcttctcagc agaccatttc aaattattaa taaatgggcc
      1801 acctccctct tcttcaagga gcatccgtga tgctcagtgt tcaaaaccac agccacttag
      1861 tgatcagctc cctaaaacca tgcctaagta caggcggatt agctatcttc caacaatgct
      1921 gaccaccaga caattactgc atttttccag aagcccacta ttgcctttgt agtgctttcg
      1981 gcccagttct ggcctcagcc tcaaagtgca ccgactagtt gcttgcctat acctggcacc
      2041 tcattaagat gctgggcagc agtataacag gaggaagaga tccctctcct ttggtcagat
      2101 tattatgttc tcagttctct ctccctgcta ccccttttctc tgcagataga tagacactgg
      2161 cattatccct ttaggaaggg gggggggcag caagagagcc tatttgggac agcattcctc
      2221 tctctctcct gctgtgacat ctccctctcc ttgctggcct ccatctttcg tctgcactac
      2281 caattcaatg cccttcatcc aatgggtatc tatttttgtg tgtgattata gtaactactc
      2341 cctgctttat atgccccctc ttccttctct ttaccccctg tgactctttc tgtactttcc
      2401 cagtgacttg ccctagccct gacccaggca ctaggccttg gtgacttcct ggggccaaga
      2461 aactaaggaa actcggcttt gcaacaggca ttactcgcca ttgattgtgc ccacccaggg
      2521 cacactgatg gagttctatc acttgcttga cccctggacc cataaaccag tccactgtta
      2581 tacccggggc actctaacca tcacaatcaa tcaatcaaat tcccttaaat ttgtatggca
      2641 ctggaacttt ggcaaagcac ttttgacaag ttgtgtctga ttggagcttc atgatagcct
      2701 tgtgacatct taggcaggat tcttatcccc attttgcaga tgaaaaaccc tgagtctcag
      2761 atttctgtgg gactgtggat ctcactggaa gcctatccaa gagcccactg tcaccttcta
      2821 gaccacatga tagggctaga cagctcagtt caccatgatc ttttgtcact ctgctggcac
      2881 accagtggca aggccagaat gcgacctctc tttagctcaa tttctgggcc tgaggtgctc
      2941 agactgcccc caagatcaaa tctctcctgg ctgtagtaac ccagtggaat gaatttggac
      3001 atgccccaat gcttctatat gctaagtgaa atctgtgtct gtaatttgtt ggggggtgga
      3061 tagggtgggg tctccatcta ctttttgtca ccatcatctg aaatggggaa atatgtaaat
      3121 aaatatatca gcaaagcaaa aaaaaaaaaa aaa
//
```

Save the above report in Macintosh Text format.

>gb|Y07637|HSGABACHL H.sapiens mRNA for putative GABA-gated chloride channel.
Length = 3153

Plus Strand HSPs:

Score = 1180 (326.1 bits), Expect = 7.6e-87, P = 7.6e-87
Identities = 236/236 (100%), Positives = 236/236 (100%), Strand = Plus / Plus

```
Query:  3861 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 3920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   829 CAGGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTG 888

Query:  3921 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 3980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   889 CCTTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGA 948

Query:  3981 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 4040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   949 TCAAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGA 1008

Query:  4041 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCC 4096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1009 CCACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCC 1064
```

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = U66661 | |
|---|---|
| *gi* | *Update Date* |
| 1857125 | 03/11/97 |

***This sequence was released by NCBI on 03/04/97***
*Disclaimer*

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA | Graphic

Links: MEDLINE | Protein | Related Sequences

```
LOCUS       HSU66661     3154 bp    mRNA            PRI       11-MAR-1997
DEFINITION  Human GABA-A receptor epsilon subunit mRNA, complete cds.
ACCESSION   U66661
NID         g1857125
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Insensitivity to anaesthetic agents conferred by a class of GABA(A)
            receptor subunit
  JOURNAL   Nature 385 (6619), 820-823 (1997)
  MEDLINE   97192095
REFERENCE   2  (bases 1 to 3154)
  AUTHORS   Davies,P.A., Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1996) Department of Cellular and Molecular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1..3154
                     /organism="Homo sapiens"
     CDS             41..1561
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /db_xref="PID:g1857126"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIA
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      725 a    886 c    686 g    857 t
ORIGIN
        1 cgcgacctcc gcgcaggtgg tcgcgccggt ctccgcggaa atgttgtcca aagttcttcc
       61 agtcctccta ggcatcttat tgatcctcca gtcgagggtc gagggacctc agactgaatc
      121 aaagaatgaa gcctcttccc gtgatgttgt ctatggcccc cagccccagc ctctggaaaa
      181 tcagctcctc tctgaggaaa caaagtcaac tgagactgag actgggagca gagttggcaa
      241 actgccagaa gcctctcgca tcctgaacac tatcctgagt aattatgacc acaaactgcg
      301 ccctggcatt ggagagaagc ccactgtggt cactgttgag atcgccgtca acagccttgg
      361 tcctctctct atcctagaca tggaatacac cattgacatc atcttctccc agacctggta
      421 cgacgaacgc ctctgttaca acgacacctt tgagtctctt gttctgaatg gcaatgtggt
      481 gagccagcta tggatcccgg acacctttt taggaattct aagaggaccc acgagcatga
      541 gatcaccatg cccaaccaga tggtccgcat ctacaaggat ggcaaggtgt tgtacacaat
      601 taggatgacc attgatgccg gatgctcact ccacatgctc agatttccaa tggattctca
      661 ctcttgccct ctatctttct ctagcttttc ctatcctgag aatgagatga tctacaagtg
      721 ggaaaatttc aagcttgaaa tcaatgagaa gaactcctgg aagctcttcc agtttgattt
      781 tacaggagtg agcaacaaaa ctgaaataat cacaacccca gttggtgact tcatggtcat
      841 gacgattttc ttcaatgtga gcaggcggtt tggctatgtt gcctttcaaa actatgtccc
      901 ttcttccgtg accacgatgc tctcctgggt ttccttttgg atcaagacag agtctgctcc
      961 agcccggacc tctctaggga tcacctctgt tctgaccatg accacgttgg gcacctttc
     1021 tcgtaagaat ttcccgcgtg tctcctatat cacagccttg gatttctata tcgccatctg
     1081 cttcgtcttc tgcttctgcg ctctgttgga gtttgctgtg ctcaacttcc tgatctacaa
     1141 ccagacaaaa gcccatgctt ctcctaaact ccgccatcct cgtatcaata gccgtgccca
     1201 tgcccgtacc cgtgcacgtt cccgagcctg tgcccgccaa catcaggaag cttttgtgtg
     1261 ccagattgtc accactgagg gaagtgatgg agaggagcgc ccgtcttgct cagcccagca
     1321 gccccctagc ccaggtagcc ctgagggtcc ccgcagcctc tgctccaagc tggcctgctg
     1381 tgagtggtgc aagcgtttta agaagtactt ctgcatggtc cccgattgtg agggcagtac
     1441 ctggcagcag ggccgcctct gcatccatgt ctaccgcctg gataactact cgagagttgt
     1501 tttcccagtg actttcttct tcttcaatgt gctctactgg cttgtttgcc ttaacttgta
     1561 ggtaccagct ggtaccctgt ggggcaacct ctccagttcc ccaggaggtc caagcccctt
     1621 gccaagggag ttgggggaaa gcagcagcag cagcaggagc gactagagtt tttcctgccc
```

```
     1681 cattccccaa acagaagctt gcagagggtt tgtctttgct gcccctctcc cctacctggc
     1741 ccattcactg agtcttctca gcagaccatt tcaaattatt aataaatggg ccacctccct
     1801 cttcttcaag gagcatccgt gatgctcagt gttcaaaacc acagccactt agtgatcagc
     1861 tccctaaaac catgcctaag tacaggcgga ttagctatct tccaacaatg ctgaccacca
     1921 gacaattact gcatttttcc agaagcccac tattgccttt gtagtgcttt cggcccagtt
     1981 ctggcctcag cctcaaagtg caccgactag ttgcttgcct atacctggca cctcattaag
     2041 atgctgggca gcagtataac aggaggaaga gatccctctc ctttggtcag attattatgt
     2101 tctcagttct ctctccctgc tacccctttc tctgcagata gatagacact ggcattatcc
     2161 ctttaggaag aggggggggc agcaagagag cctatttggg acagcattcc tctctctctg
     2221 ctgctgtgac atctccctct ccttgctggc tccatctttc gtctgcacta ccaattcaat
     2281 gcccttcatc caatgggtat ctatttttgt gtgtgattat agtaactact ccctgcttta
     2341 tatgccaccc tcttccttct ctttgacccc tgtgactctt tctgtaactt tcccagtgac
     2401 ttcccctagc cctgacccag gcactaggcc ttggtgactt cctggggcca agaaactaag
     2461 gaaactcggc tttgcaacag gcattactcg ccattgattg gtgcccaccc agggcacact
     2521 gtcggagttc tatcacttgc ttgacccctg gacccataaa ccagtccact gttatacccg
     2581 gggcactcta accatcacaa tcaatcaatc aaattccctt aaatttgtat ggcactggaa
     2641 ctttggcaaa gcacttttga caagttgtgt ctgattggag cttcatgata gccttgtgac
     2701 atctttaggg caggattctt atccccattt tgcagatgaa aaccctgagt cacagatttc
     2761 tgtgggactg tggatctcac tggaagctat ccaagagccc actgtcacct tctagaccac
     2821 atgatagggc tagacagctc agttcaccat gattctcttc tgtcacctct gctggcacac
     2881 cagtggcaag gcccagaatg gcgacctctc tttagctcaa tttctgggcc tgaggtgctc
     2941 agactgcccc caagatcaaa tctctcctgg ctgtagtaac ccagtggaat gaatttggac
     3001 atgccccaat gcttctatat gctaagtgaa atctgtgtct gtaatttgtt gggggggtgga
     3061 tagggtgggg tctccatcta ctttttgtca ccatcatctg aaatggggaa atatgtaaat
     3121 aaatatatca gcaaagcaaa aagaaaaaaa aaaa
//
```

Save the above report in Macintosh Text format.

>gb|U66661|HSU66661 Human GABA-A receptor epsilon subunit mRNA, complete cds.
Length = 3154

Plus Strand HSPs:

Score = 1170 (323.3 bits), Expect = 5.2e-86, P = 5.2e-86
Identities = 234/234 (100%), Positives = 234/234 (100%), Strand = Plus / Plus

```
Query:  3863 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 3922
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   824 GGTGACTTCATGGTCATGACGATTTTCTTCAATGTGAGCAGGCGGTTTGGCTATGTTGCC 883

Query:  3923 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 3982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   884 TTTCAAAACTATGTCCCTTCTTCCGTGACCACGATGCTCTCCTGGGTTTCCTTTTGGATC 943

Query:  3983 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 4042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   944 AAGACAGAGTCTGCTCCAGCCCGGACCTCTCTAGGGATCACCTCTGTTCTGACCATGACC 1003

Query:  4043 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCC 4096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1004 ACGTTGGGCACCTTTTCTCGTAAGAATTTCCCGCGTGTCTCCTATATCACAGCC 1057
```

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

**Other Formats:** FASTA | Graphic

```
LOCUS       HSGABRE1      556 bp    DNA             PRI       03-JAN-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exon 1.
ACCESSION   U92281
NID         g2735345
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 556)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1..556
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     5'UTR           <162..200
                     /gene="GABRE"
     exon            <162..256
                     /gene="GABRE"
     mRNA            join(<162..256,U92282:64..281,U92282:730..797,
                     U92283:301..521,U92283:1577..1659,U92283:2966..3103,
                     U92283:7082..7234,U92283:7375..7574,U92283:7858..>9631)
                     /gene="GABRE"
                     /product="GABA-A receptor epsilon subunit"
     CDS             join(201..256,U92282:64..281,U92282:730..797,
                     U92283:301..521,U92283:1577..1659,U92283:2966..3103,
                     U92283:7082..7234,U92283:7375..7574,U92283:7858..8241)
                     /gene="GABRE"
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /db_xref="PID:g2735345"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
     intron          257..>556
                     /gene="GABRE"
BASE COUNT       81 a    203 c    189 g     83 t
ORIGIN
        1 tccccggctc cccaccgcag cagccgtcac gtcgtcggag atttccatcg gggcgggcct
       61 ggggcgggga gcgcgggacg gggcggggcg agtgggagga gtgaaagttg gagcccagca
      121 aaagcctccg ccccgcgctc agtgcggcca gagcgtgagc cgcgacctcc gcgcaggtgg
      181 tcgcgccggt ctccgcggaa atgttgtcca aagttcttcc agtcctccta ggcatcttat
      241 tgatcctcca gtcgaggtga gtctccatcc cgggacccgg gagcccttcg cgcccagctc
      301 cctctccccg ggagccggga cggctcccgg gaccccagcg gccccgcgtt cctcgagccc
      361 cgcgcccgct ttgccccggc cctaccgcgg gctggccgag tcccgcgtcc cctcgatgcg
      421 cgccggcctc ggcccgcctc actgtaggat gggctcccgg ggtccttgag ggggagctcc
      481 aaaaggaaga caggacgcca gaaggaagac gggactccag ttcgcggatt cccgctctca
```

```
      541 aaagcactgc ggtggc
//
```

Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = U92281 | |
|---|---|
| *gi* | *Update Date* |
| 2733345 | 01/03/98 |

***This sequence was released by NCBI on 01/01/98***

*Disclaimer*

NCBI Entrez **Nucleotide QUERY** BLAST Entrez ?

**Other Formats:** FASTA Graphic

```
LOCUS       HSGABRE2     1097 bp    DNA             PRI       03-JAN-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exons 2 and 3.
ACCESSION   U92282
NID         g2735346
KEYWORDS    .
SOURCE      human.
  ORGANISM  [illegible]
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1097)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1097)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1..1097
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     intron          <1..63
                     /gene="GABRE"
     exon            64..281
                     /gene="GABRE"
     intron          282..729
                     /gene="GABRE"
     exon            730..797
                     /gene="GABRE"
     intron          798..>1097
                     /gene="GABRE"
     mRNA            join(U92281:<162..256,64..281,730..797,U92283:301..521,
                     U92283:1577..1659,U92283:2966..3103,U92283:7082..7234,
                     U92283:7375..7574,U92283:7858..>9631)
                     /gene="GABRE"
                     /product="GABA-A receptor epsilon subunit"
     CDS             join(U92281:201..256,64..281,730..797,U92283:301..521,
                     U92283:1577..1659,U92283:2966..3103,U92283:7082..7234,
                     U92283:7375..7574,U92283:7858..8241)
                     /gene="GABRE"
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /db_xref="PID:g[illegible]"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      281 a    266 c    239 g    311 t
ORIGIN
        1 ggcactagct ggggccccta cagagtgcag ggcagagctt cattttcgt ttgaatgtta
       61 tagggtcgag ggacctcaga ctgaatcaaa gaatgaagcc tcttcccgtg atgttgtcta
      121 tggcccccag ccccagcctc tggaaaatca gctcctctct gaggaaacaa agtcaactga
      181 gactgagact gggagcagag ttggcaaact gccagaagcc tctcgcatcc tgaacactat
      241 cctgagtaat tatgaccaca aactgcgccc tggcattgga ggtgaggagc agaacgacgt
```

```
      301 tcttcccctc ctagagggtc caggggttga gggcataggc atggagaatg cacctgggca
      361 gtaacagagg gtgccatgct catggacagg aacatctgct attgacctgt caggtaagag
      421 atattaactc tattctcagc agtgtcattg accttgatca agacttttcc cttctctcgc
      481 cctcagtttt tccagtggta aaatgagagg actaaactag attgttgatc ttcaagatgt
      541 gtgtccaatt cttaacagtc cgtgagcttg gttttgccat gaaagaataa ataaagaaat
      601 aggattagat gctgaaactg tgtggtccaa cacttacttg actccccttt catcccctct
      661 gaccacttcc tcccccgtcc catgcgcctg tttgacactt accctctgct gcttctgctt
      721 cccttataga gaagcccact gtggtcactg ttgagatctc cgtcaacagc cttggtcctc
      781 tctctatcct agacatggtg agtactaagc ttttttagta ctatttccta gcccaggggc
      841 tgacctatgg gaccttccac agacttctgc tttctgctct gtacttctgt aacaactcca
      901 ataatttatt ttctggaggg agaaagggat tttttaacca ctggtttgag aatgagactg
      961 gaaaaggtaa gtcccttgct acttgaagag gatcttcaga atcatgacca tatcttccag
     1021 ttttttcatt caaaatagaa ataataaagc aatgttaaac accacaatgg actgcctctt
     1081 ttcttctgat aattatt
//
```

Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = U92282 | |
|---|---|
| *gi* | *Update Date* |
| 2755346 | 01/03/98 |

***This sequence was released by NCBI on 01/01/98***

NCBI Entrez **Nucleotide QUERY** BLAST Entrez ?!

**Other Formats:** FASTA | Graphic

```
LOCUS       HSGABRE3     9631 bp    DNA             PRI       03-JAN-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) gene, exons 4-9, and
            complete cds.
ACCESSION   U92283
NID         g2735347
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9631)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1..9631
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     intron          <1..300
                     /gene="GABRE"
     exon            301..521
                     /gene="GABRE"
     intron          522..1576
                     /gene="GABRE"
     repeat_region   1095..1134
                     /rpt_type=tandem
                     /rpt_unit=ttttg
     exon            1577..1659
                     /gene="GABRE"
     intron          1660..2965
                     /gene="GABRE"
     exon            2966..3103
                     /gene="GABRE"
     intron          3104..7081
                     /gene="GABRE"
     stem_loop       3230..3314
                     /gene="GABRE"
     stem_loop       4283..4365
                     /gene="GABRE"
     exon            7082..7234
                     /gene="GABRE"
     intron          7235..7374
                     /gene="GABRE"
     exon            7375..7574
                     /gene="GABRE"
     intron          7575..7857
                     /gene="GABRE"
     exon            7858..>9631
                     /gene="GABRE"
     3'UTR           8242..>9631
                     /gene="GABRE"
     gene            order(U92281:<162..556,U92282:1..1097,1..>9631)
                     /gene="GABRE"
     mRNA            join(U92281:<162..256,U92282:64..281,U92282:730..797,
                     301..521,1577..1659,2966..3103,7082..7234,7375..7574,
```

```
                     7858..>9631)
                     /gene="GABRE"
                     /product="GABA-A receptor epsilon subunit"
     CDS             join(U92281:201..256,U92282:64..281,U92282:730..797,
                     301..521,1577..1659,2966..3103,7082..7234,7375..7574,
                     7858..8241)
                     /gene="GABRE"
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /db_xref="PID:g[illegible]"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT     2267 a   2381 c   2249 g   2734 t
ORIGIN
        1 tgcatgatgt gaggacctag ctccccttgc tcacggtaat caagcagggc atgactgact
       61 tctcatttgg gatcattagg cttggtaacc tctgagttcc cttctagttc tgacattgga
      121 agagtctttg agcagagaga agggacctca tctgactcct gcttcctggt ctagtgctca
      181 atgcattcca ccacattgcc tttaggattc taggttaggg agtggcaaac aatatgtttg
      241 catgtgaatg tccttttttct gttcatcccc aagtatgtgc ttttctgtcc ttcccaccag
      301 gaatacacca ttgacatcat cttctcccag acctggtacg acgaacgcct ctgttacaac
      361 gacacctttg agtctcttgt tctgaatggc aatgtggtga gccagctatg gatcccggac
      421 acctttttta ggaattctaa gaggacccac gagcatgaga tcaccatgcc caaccagatg
      481 gtccgcatct acaaggatgg caaggtgttg tacacaatta ggtatgtcaa gcctctggag
      541 tctcacttcc tggaattctc tctccccttc tgataatttt agctaaagat ccatgggcag
      601 agatctcatc ctgaatgata cctctaaggg cctgtccagc tttcctagac catgagctca
      661 gccccccttat gtaacagata tagaggcctc aaaatagaaa gatattgctt aaagccacac
      721 accaagtttg tggcagagct ggaactggta ctcagttact tggctccgag tccagagctc
      781 cctcaactag gatgtgccag tatgactgca ttatctagac aattccatcc tacgtgggca
      841 ctcgatacaa agatacgtcc acagtggtgg aattgttcag gcagagcagc agcacgtagt
      901 ggcaaaggta cctaagatca agttggatac ttgaattccc agcaggggaa ggttgtgtgt
      961 ggggatagca gggaggatgt tggcagttcc tggaaactag ggtgggcgag aaaacaaaag
     1021 ccgatcgaag ttgctccata cgtttctcta atgatggagc ccagagtaac cagatacttc
     1081 taagctgttt gtttgttttg ttttgttttg ttttgttttg ttttgttttg ttttctctct
     1141 tgttatctct cctttgagct ttttgtctta aattctagcg aggtccaggc acggtggctc
     1201 acgcctgtga tcccagcact ttgtgaggct gaggcaggca gatcacttga ggtcaggagt
     1261 tcgagaccag cctggccatc atgggaaaac cctgtctcca ctaaaaatgc aaaaattagc
     1321 agggtgtgct ggcactaatt ccagctactc gggaggctag ggcatgagaa ttgcttgagc
     1381 ctgggaggca agaggctgca gtgagctgac atcacgccac tgccctccag cctgggtgac
     1441 agagtgagac tctgtctcaa acaaacaaag aaaaaaattg actctggcca ttcattggtg
     1501 gtagtcccta gaccaaagct gggtggatac ggaagtgctt agggccagcc tgatgaggct
     1561 cctttctccc ttccaggatg accattgatg ccggatgctc actccacatg ctcagatttc
     1621 caatggattc tcactcttgc cctctatctt tctctagctg tgagtacctt cttaagtttc
     1681 tggggcccca gaaacatgct gggctccttc tttttctcat ccttgccatt tacatttttc
     1741 tgcctctgct tttcttctaa aatgctgcca aggttgtgca ggacttccat cctccaccct
     1801 catttccttt cctgccaaca atactgtgtt gctcatccct tccacgtgcc tctgaagcgt
     1861 atctcaagta tgtctgctcc tctccatctc cactggcact accttggttt aggcctttgt
     1921 tatcttccac ctggactttt gccacatctt cactttgaaa ctgcacatgt ccaaaatgaa
     1981 attcattgtc tcctccaaac ctctaccacc aaaacaagtg tgttgcttct gggttcccat
     2041 ctgtctcatt gaagaggacc atcactcacc cagttgcgca aatcaagaac tttgatgttt
     2101 cctctccctc acctcctgca tctaatcaat cagcacatcc tgttggtgtt tcctcccagt
     2161 ctctatcgat gctgtctatt tctctgcacc ctgtacagct ttgacttcca cctgcattaa
     2221 tttaattctg cctggattac tacactggcc tccttgacaa catgttgtcc tcacagaagg
     2281 accagagtga cctagctgaa gggtcaccta ggttgggtca cttcttagtc tcgaatctgc
     2341 cgttaactct catggatcaa tttgaaattc cttagaatga acctcaaggc cattcatgaa
     2401 ctggaccctg ccacccaatc ctgtgcacct catcctctgt gagctagcca tcctgaactt
     2461 ttgtcctttc cacaatacac caggtgtttc acctttctat actgcccctt aaccccttca
     2521 acctcattct tattgagaat atttacttga gtttcaagat ttaatgggaa tatcacctgc
     2581 tttatgaagt cttttctgag tatgtcccca agtgaccttt atctactttg tttccccgct
     2641 gttctgtgga cttaggtttt tcagagctcc tccaaaaatc acagtagtat actcactgtc
     2701 ttataaaatt aaatgtgatt gcttgagggt agggttcatg ccttgctcat ctctgtattt
     2761 ctggcctagg gcctgatact gaggaatgct cagtaaacgc actcattgaa tggacttcaa
     2821 caatgaggta agagaggcaa ggtcccacag ctggtgaggc cagagacagg actccaaggc
     2881 attgtgcagg ctgagttcat gctattggag acctcaggtg ggcttccaag tctcatagga
     2941 ccctctttct cacattcctt tccagtttcc tatcctgaga atgagatgat ctacaagtgg
```

```
3001 gaaaatttca agcttgaaat caatgagaag aactcctgga agctcttcca gtttgatttt
3061 acaggagtga gcaacaaaac tgaaataatc acaaccccag ttggtaagcg tgccagggct
3121 tggcggaagt ccaggaaggt ggtagggatg attggagatg gccatccata caaatgcttt
3181 gcagtcatcc cgtgcaaaca ttgtaagaca tggctcctgt cttataattg ctaagcactt
3241 acaactgttt gcagaggaaa ctgagacttt gtaactatgt ctcagtctca tctgcaaaga
3301 agtaagtgct ttgccaagct ccttgagagg ttaggtaagt agataaagtt ctgctgctgt
3361 cggaatgtgc agctggcttt ttcatgcaga cccttcagtt tcgaggttac aactctgacc
3421 tctttggatg actttgggga atggagctcg tgtgagttct ccatacccag aaccaatcca
3481 gtctggttga atgggaagca aagtccattg tagtgggagg tggaggctag agttctaatg
3541 tcagctagtt taaggctggg aaagtctgga ggaagttaca gcagctacac tggctgctgc
3601 attgacattt atcttaaagg aacaagtctg aaaagcacag attcttatca aaggcttcat
3661 ggtggattcc acatagacat agtggccact ggttttctga ccttttctct gacaaagact
3721 aaaggggaag gtcctgggta tcttacactt cagctcccaa ttagatgtga gcaccttcac
3781 ttatgttcct aggtgacctg aatgaggagc caagggacct ccccagggta gctcccagag
3841 caaccctgga aacactcttc acacatcctg accaagttca gggcagtgaa ggcactgccc
3901 tcatcgtttc cagaatgtgg atggagccag tcacccaacc agccatttgt cgtgagaggc
3961 atcttgttct gctaccatgt gactaggcag aaaatctgct tttgtttcat ttattgagtc
4021 agtctctgga tgagggaaag ctcatgctca tgtggctaga gctttgcttg cacagtatta
4081 ggcaggggca gagggctggg ctaccttaaa aatacttgcc ctttttcttg gggactctgg
4141 ggaagcggtt ttactacctt tgacttggga gccttgctct tctgccagct aaccatgggc
4201 ctgcctcttg gttttctgca cctcagcttt tcccggatag gtggggaccc atcatcaaaa
4261 gtgacagaga agataaggcc caggggcttt caagtcacta gtggttccgt ttagtagatg
4321 attgtgcatt gtttcaaaat ggtgccctag tgactacaaa gccccagagc cagcatcatc
4381 atcaaagcaa tgacagtagg taagcaccag acctccttgg gagtgaggag gattcttgag
4441 gagaaaagag gtcttctttc tcctctgctg gagactagtt gatctggaga cgtggttcct
4501 tcaatgtcag agttatcttt gggactggtc tcaaactctt ccagttgggc cctggggcag
4561 gtctctccat ctggagcata cttacgtgct cggcgattaa gggttcagaa tgcagtggta
4621 gcctgctact ctggccatct tggaccttga tccagagaat ctctgcttca ggagcttcta
4681 agagagtcca gccctgcctc cagagagagg cttgcccttc actgatggct gtggagcctc
4741 tgatggaata ttattgctgg tcaggaattc actgtcttac aaggaggttt ccttcttctc
4801 tagacagttc tgttcatcaa aaaactctcc ctgttcttct gaaattggag tctctggaag
4861 ttccacacat taagcttagt tctttttcct tggaactgtc caggttacat tagtccagcc
4921 actgtttcac aggaccgaga ttaaacgatc aacatcatca ttcccggcat ggatcatagt
4981 ctgttgtagt ctacatagcc ctagtttatt tttcttccct tattcttcaa agctttgggt
5041 ccattcattc ttctagtccc agtcctctgg acatggtcta tttaattgtg tccctctgac
5101 actgcagtga ccaaccatga tctggtcaaa gaggataaga gtttgagcag aaaaccatct
5161 ttagcatata ttttttttgct ttggttcatc agccccagat atattgtttt ccttacccgt
5221 gcttctctca ctcctcaaga agaagaaagt gtgtgttagc atctttctct tgtccttcaa
5281 gacaaattgg catctcttga cgagcggaga aggttctttt ttggccagaa taaataaaat
5341 taaaatagaa tcatccaaca gaataataaa tcttcgtgca acaagaatat attatataaa
5401 cccagcaatt ttgcagggcc tgggtataac taattagaag tgtcttaaat tgcagtcaag
5461 atcccacggc aagaggactt ttgataaata cattctggcc agtaggcaag tgcgagggtg
5521 gtccgtgcag cagctctgga ggagttctat cccaaagcta tactcaacac acaggtttcc
5581 cactgacaac aggtcgctcc cttgccttct tccagaagaa tctgagaagc tttgctcctt
5641 gagtttcagt gctgccaagg tgagtacgaa aggctgctct tctcattcag ctccagccca
5701 cccagacctg ctgggcagtt gatccacttt ccaaaatagg aggacacacg gacaggttag
5761 tgttctggtc tgctttacaa agctgttgcc tgacaggagc aagagttgct gagtgtctgc
5821 tgggttccag gctgttctga gcttggatgg gcaggggcta agccacaggg cctgcatgag
5881 ccctgccttg aagggactta aaagacgacc taattatagg cctaggaatt ttacagtatt
5941 gcaactgcaa tgtgatgctg aaagtggaaa atgatgtcct gggctcagag aaaagcccac
6001 accagcctgg gagtcatgat agcagcagag tgcttgggga gggtgtgtca gagcataaag
6061 cagcatgaat gctacaaaag aagatgccaa ctagagatat aggttgtcat caggtcccgg
6121 aggagccatg accgtctagc tgagagccat gaccaaggac acaatgtcca agtgactgtg
6181 aggacctcag tctgccctgt ggatgtgtat gccacagacc tgacttctgg agggctgact
6241 gaaatgttca ttttaagctt tttcttctct ttccctgaaa cactcagttt gggttagggg
6301 tcatagacta agaccaaaga gtccagggtt agaatcttgg tgtaaaattg caggccatct
6361 caggaaatct gtgagcagat gggattggct ttgggtaagg tgcgtgtgga aaatgtcagt
6421 gggagccggg tcatggtggg cctttagcat cagattccag agtgcagata gtctgtatag
6481 ctcatgtgaa acagggagcc accaaaactt tggggagcag gctagtgccg gttttgacca
6541 cctgtggagc agtgctcact cacgaaggca ttttgccatc acatgaatgt gcagaaagga
6601 ggccaaaagc attctgtgct tctccaccac agcacagact tccctagtct catttgctga
6661 gagtagacat tctgagggcc agcagtgcag gtgtgatgtg cctcagaggg tatgaagccc
6721 ttagtcagcc atctggatat cagctgcgtg ggcatgatat ctagaaggct aattgatttt
6781 ttcactttca cctgactctc ttgccaacct gcagagacag acattgggtg taggacagtg
6841 aactgagaag gaagctatta agattctggc cttggcttag ctctcaactg gccattggtc
6901 ttgcagtaag tctttttttct gggcttcttc tggtcctatt tgtatgtatt gcattgtcac
6961 atcatgcctc tatcctaggg aatactgtga gctgaaaaat gagaccctta ctgttcacgt
7021 cctgctaagg gggaccgtcg tgtcagcact gtaatgcagt gatgtttttt gtgtctttca
7081 ggtgacttca tggtcatgac gattttcttc aatgtgagca ggcggtttgg ctatgttgcc
7141 tttcaaaact atgtcccttc ttccgtgacc acgatgctct cctgggtttc cttttggatc
7201 aagacagagt ctgctccagc ccggacctct ctaggtaaga ggagaaacag gtatacgcat
```

```
     7261 aggcacatgg ctgggagttg gctgggccag ggcagagttg ccttgtcatg gagtctttta
     7321 accaatgtcg cacataggtc aggagctgag cccatcactc ttgtgctctt gcagggatca
     7381 cctctgttct gaccatgacc acgttgggca ccttttctcg taagaatttc ccgcgtgtct
     7441 cctatatcac agccttggat ttctatatcg ccatctgctt cgtcttctgc ttctgcgctc
     7501 tgttggagtt tgctgtgctc aacttcctga tctacaacca gacaaaagcc catgcttctc
     7561 ctaaactccg ccatgtatga gctgggtatg ggagtggtgg caaggctttg gagtgtagag
     7621 acatgctagc aagggtactg gggttatggc acatgggtgg tcagcttgct gagtgatgga
     7681 atgttaccca gggtggtggc ggggttgaat caacttcctg atgtaatggt gagaagttgg
     7741 aggagagaag ccaagatatg gtgtgccaaa gacagtttcc agaaaatccg gaggcagcac
     7801 ttagacttgg gttatcttcc cttgactttt ccccacttct ttccttgtcc attttagcct
     7861 cgtatcaata gccgtgccca tgcccgtacc cgtgcacgtt cccgagcctg tgcccgccaa
     7921 catcaggaag cttttgtgtg ccagattgtc accactgagg gaagtgatgg agaggagcgc
     7981 ccgtcttgct cagcccagca gccccctagc ccaggtagcc ctgagggtcc ccgcagcctc
     8041 tgctccaagc tggcctgctg tgagtggtgc aagcgtttta agaagtactt ctgcatggtc
     8101 cccgattgtg agggcagtac ctggcagcag ggccgcctct gcatccatgt ctaccgcctg
     8161 gataactact cgagagttgt tttcccagtg actttcttct tcttcaatgt gctctactgg
     8221 cttgtttgcc ttaacttgta ggtaccagct ggtaccctgt ggggcaacct ctccagttcc
     8281 ccaggaggtc caagcccctt gccaagggag ttgggggaaa gcagcagcag cagcaggagc
     8341 gactagagtt tttcctgccc cattccccaa acagaagctt gcagagggtt tgtctttgct
     8401 gcccctctcc cctacctggc ccattcactg agtcttctca gcagaccatt tcaaattatt
     8461 aataaatggg ccacctccct cttcttcaag gagcatccgt gatgctcagt gttcaaaacc
     8521 acagccactt agtgatcagc tccctaaaac catgcctaag tacaggcgga ttagctatct
     8581 tccaacaatg ctgaccacca gacaattact gcatttttcc agaagcccac tattgccttt
     8641 gcagtgcttt cggcccagtt ctggcctcag cctcaaagtg caccgactag ttgcttgcct
     8701 atacctggca cctcattaag atgctgggca gcagtataac aggaggaaga gatcctctc
     8761 ctttggtcag attattatgt tctcagttct ctctccctgc tacccctttc tctgcagtta
     8821 gatagacact ggcattatcc ctttaggaag agggggggc agcaagagag cctatttggg
     8881 acagcattcc tctctctctg ctgctgtgac atctccctct ccttgctggc tccatctttc
     8941 gtctgcacta ccaattcaat gcccttcatc caatgggtat ctatttttgt gtgtgattat
     9001 agtaactact ccctgcttta tatgccaccc tcttccttct ctttgacccc tgtgactctt
     9061 tctgtaactt tcccagtgac ttcccctagc cctgacccag gcactaggcc ttggtgactt
     9121 cctggggcca agaaactaag gaaacttggc tttgcaacag gcattgctcg ccattgattg
     9181 gtgcccaccc agggcacact gtcggagttc tatcacttgc ttgacccctg gacccataaa
     9241 ccagtccact gttatacccg gggcactcta accatcacaa tcaatcaatc aaattccctt
     9301 aaatttgtat ggcactggaa ctttggcaaa gcacttttga caagttgtgt ctgattggag
     9361 cttcatgata gccttgtgac atctttaggg caggattctt atccccattt tgcagatgaa
     9421 aaccctgagt cacagatttc tgtgggactg tggatctcac tggaagctat ccaagagccc
     9481 actgtcacct tctagaccac atgatagggc tagacagctc agttcaccat gattctcttc
     9541 tgtcacctct gctggcacac cagtggcaag gcccagaatg gcgacctctc tttagctcaa
     9601 tttctgggcc tgaggtgctc agactgcccc c
//
```

Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = U92283 | |
|---|---|
| *gi* | *Update Date* |
| 1735347 | 01/03/98 |

***This sequence was released by NCBI on 01/01/98***

Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

Links: Protein

```
LOCUS       RNU92284     7479 bp    DNA             ROD       01-JAN-1998
DEFINITION  Rattus norvegicus GABA-A receptor epsilon subunit gene, partial
            cds.
ACCESSION   U92284
NID         g2735328
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  [redacted]
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 7479)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7479)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1..7479
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     mRNA            join(<1..200,895..977,2138..2275,5938..6090,6207..6406,
                     6654..>7479)
                     /product="GABA-A receptor epsilon subunit"
     exon            <1..200
                     /number=4
     CDS             join(<1..200,895..977,2138..2275,5938..6090,6207..6406,
                     6654..7034)
                     /codon_start=1
                     /product="GABA-A receptor epsilon subunit"
                     /db_xref="PID:g[redacted]"
                     /translation="FYQTWYDERLCYNDTFETLILHGNVVSQLWIPDTFFRNSKRTQE
                     YDITIPNQMALIHKDGKVLYTVRMTIDARCSLHMLNFPMDSHSCPLSFSSFSYDEHEM
                     IYKWENFKLKIDAKNTWKLLEFDFTGVNNKTEIISTPVGDFMVMTFFFNVSRRFGFIV
                     FQNYIPSSVTTMLSWVSFWIKIEAAAAARASVGVSSVLTMATLGTFSRKNFPRVSYLTA
                     LDFYIAICFVLCFCTLLEFTVLNFLTYNNIERQASPKFYQFPTNSRANARTRARARTR
                     ARARARARQQQEVFVCEIVTYEENAEEGYQWSPRSRRPQCPWRRCGRSYVCFRVLRKY
                     FCMVPGCEGNSWQRGRICIHVYRLDNYSRVLFPITFFFFNVVYWVICLNL"
     intron          201..894
                     /number=4
     exon            895..977
                     /number=5
     intron          978..2137
                     /number=5
     exon            2138..2275
                     /number=6
     intron          2276..5937
                     /number=6
     stem_loop       2412..2496
     stem_loop       3389..3472
     exon            5938..6090
                     /number=7
     intron          6091..6206
                     /number=7
     exon            6207..6406
                     /number=8
     intron          6407..6653
```

```
                /number=8
     exon       6654..>7479
                /number=9
     3'UTR      7032..>7479
BASE COUNT     1931 a   1620 c   1557 g   2371 t
ORIGIN
        1 ttctaccaga cctggtatga tgagcgcctc tgttacaatg acacctttga gacacttatt
       61 ctacatggca acgtggtgag ccagttgtgg atcccggata ctttttttag gaattctaag
      121 aggacccaag agtatgatat caccataccc aaccagatgg ctctcatcca taaggatgga
      181 aaagtgttgt acacagttag gtatgtcaag cctttagtgt ctcactttct agggctctct
      241 cactcttcca gaaaatttta gctagggact cctaagtaaa tatatcattc tgaataatat
      301 tcctaaaacc ctgtgcagct tttctagatc aggaattcaa cctcttcctg tgcaaatata
      361 agacactgag atattaaata aaagatttta aagatgcatg ccaagtgttt tggtaatcat
      421 ggagctgtat ttgccccaca gtctagaagg taggtgctgg cctgactgta ttagtagata
      481 attccatccc aaatgggcat agtatttaaa gacacgccca cagtgacaga attgtccagg
      541 cacagtataa atacatcggt ggaaaagtat tcaggactag gatacataaa ttgaatgcct
      601 ggaaggagat gcttgtgtca gcaatatggg atgtggaggt ggtgcaaagt agcacaggac
      661 tagagcactg cacgaacaag aaagaaaaat caatctaggc tggcccatgt acttctttga
      721 tgatgtagcc tagtagtcag attttagaag ttcttcttcc tctctttgta tcattccttt
      781 gggctttttg tcttaaattc tactaatggc actcattaga tatgatacct ggtcaatgtt
      841 gagtagatat cagtgcaaag agccagccta atgaggctcc tttctccctt ccaggatgac
      901 cattgatgca agatgctcac tccacatgct caattttcca atggattctc actcttgccc
      961 tctgtctttc tctagctgtg agtaccttct taggtttctg gggatccaga gatatgctgg
     1021 gccccacttt tgctcatctt tgccttttac atttttctgc ttctgcttgt ttcctgtgat
     1081 ggtgccaggg ttgctataag cctccatttt ccatcatcac ccctttttct gtaagcagtg
     1141 ctgtgtgtgt attgctttgg ctttatgttg aattcttccc tcacccttgc tctaccttaa
     1201 gctagtcacc tgcttctgaa gtatatctga agtatgcctg ctcctctcca tctctgcctt
     1261 gatgcagggc tttaatcatc ttctgcttgg acttctacag taccttcact ttgaaacaga
     1321 gtgtgtctta agctaaattc atttttttct tcccaacacc tgcctccaaa gcaaatgtgt
     1381 cgcttctgtg ttgcctcatt gaagggtgcc atcatttacc cagctaccca agccaagaac
     1441 tctgacagcc ccattcattg acctcctaca tctactcagt tcacacatcc tgttggtgtt
     1501 ccctccaaat ctctattgat ctcacctcca tctctgcatt ctgactatta ttagctttca
     1561 ttcctcattt caaatgtgtt ctttgctcgc ctggatcaat tctaaatgcc ttaaaatgaa
     1621 cctcaaatcc cttcatgagc tgaccctgct gcttcctgct atacaaccta tctgtgaaat
     1681 agtctcccta aagttttgct gtttccacat tcacctttct gtgcttccct ttcaccttct
     1741 tcaacctcat ctctattgag aatgtttatt ttcaaaactt aaagtgaatg ccccatgctt
     1801 taggaagtgg gtcccaagag atctttccct attttgccaa ttgttccatg ggtagagatt
     1861 tttcagagca acccccaaac tcacaattgt atatggcctt actcaatgca atgtgaatgc
     1921 tggagggtag gttcacgcct tactcatctt tgcatccgaa gcccagggca aatgtactta
     1981 ttgaatgcac ttcaacaact gggccaaagg cagggtctca aagctggtga agccaaagtc
     2041 aaaagtccaa aacatggctc aagctagcac catgcttgtg gggccctcaa ctgggtttcc
     2101 cagtctcatt cattcctctt ttccacattg ttttcagttt cctatgatga gcatgagatg
     2161 atatacaagt gggagaattt caaactcaaa atcgatgcga agaacacttg gaagctattg
     2221 gagtttgatt ttacaggagt gaacaacaaa actgaaatca tctccacccc agttggtaag
     2281 tgtgcagtgg gagctagagc tgggcagagt ctgagggtgt agtaccaaca actggaagtg
     2341 gctatttgta ccaatgctat gtaaagagct tatggaaaca ctgtctagga catcgcttct
     2401 ctctcatata tgctaaacac ttacaactgt ttgcagagga aactgagact tcatagctat
     2461 gtctcagtct catctgcaaa gaagtaagtg ctttgccaag ccccttgaag gacggggtaa
     2521 gtagatatat gtttgtaacc ttcagtatgt taatctacct tttgagtttt agatcttttg
     2581 tatttaattt ctttcttata tcactgacta acttagacaa cattggggag gggtactctg
     2641 tgtgatttta ccaaatcctg aaccaggtca agttggttga gtgggaagga agaccaccct
     2701 agcaggaggt agaagtggaa actagagtga caatggcggc tagtagggat tgaggagtct
     2761 gcagatggtt actcaggtgc aatggctaca gtaatattat cttaaaggag caactgtgaa
     2821 gagtacatat tttcaccaga ggcttcagag tggaatcaac ataaacatgt tttttcctcc
     2881 tgatcttgtt cctgacaagg ataatagggg cagattctgg gtctcttaac ttgtatctcc
     2941 caaatagatg tgagcatctt tgcttgtatt cctaggtgat ctgaatgagg agccaataaa
     3001 tcttctcagg gtacctctga gagcaaccct ggaccttctt cacatgtact gacaagaatg
     3061 tggatggatc aggtcaccca gccagacttt tgacatttat tttgctttgc ttctgtgtga
     3121 tgatgacata aaaaaatctg ctattgctac tgttggtcac tcggtgaggg gcagcttatg
     3181 ctaacccaac taaagctttg cttatacaat actaggcagg gatgggtgct gcttgtcctg
     3241 ttcctgggac tctgagaaag ccttcttgct tgctttgact tggggttctt gttcttcttc
     3301 tacataaatg tgggcctgcc tcttagtatt cagtttgtcc agataggtgg agcctcatca
     3361 tcagaagtga cagaagagac aaggttcagg ggctttcaag tcactagtgg ttccgtttag
     3421 tagatggttt ttgcattgtt tcaaaatggt gccctagtga ctacaaagcc ccagagccag
     3481 catcatcagt gaagcaatgt cagtaggtaa gcaacatctc ttactgtgga gaaagaaata
     3541 ggtcttcttt tttcattgac tagagactac ttattctgaa ttcatactgt cttcactgtc
     3601 agttatttttt gagtcaggtt ccaactctcc cagtttgacc ctggggcact tctttctagc
     3661 tagaacacac atgtactcat ttttcagggt ttaaatgcag cagtgccctg caacttgggc
     3721 catcttggac cttacagcag agtttctgct tcaggagctt ctcagaaagt gcagccttgt
     3781 ctgtagtaag taaaccatcc ttcactggtg gctgttgagc ctctgaggaa atcttgccac
     3841 gatcaagagg tcagcatctt acaaggagat tattttcttc cctagacgtc tctttccatc
```

```
3901 agaaaattct tcttgctcat ctaaaatggg agtttctgga acatttaccc atcagatcta
3961 gttctttttc ccctataact acccagttta cattaattta aggtactctt tcaaaagtca
4021 aatgtaaaga tctagggtta acattagagc acacatttgt attctattgg gactctcctc
4081 cctagttcct tttcttctct tgttcttcag ttcactagtc ctctgggcag tcttttaatt
4141 gtgtcttttg acagtgcagc catcaactat gatctggaca aagcaggtaa gaaccaaagt
4201 catctttaat ccattttgtt ttggtttggc tttcagtcct agatacctct cttccattgg
4261 tattgcttct tcaatcatca gaatgaaaga aacacttatt agtatccttc tcttgtccaa
4321 tttccagctt ttagtaaata aaacatttct tctttaatca gactgactaa aatttaaaga
4381 atgagaaacc caacagcaca atgcatcttg tgacatacat attaagggag tttttaatca
4441 cagtcaagtc tccaggacag aaagaataat aatttggtca ttctggctag tagcatagaa
4501 tggtttctgg tgcagtgccg gaggcattct agtattcagg caggaagttt cccactgacc
4561 ataagctact tatttgcctt tctctgaaga acctgagaag ctttgttcct ccaaggtcaa
4621 gtctcctaac actaggagga aaggttgctc tcgatcttca cggcccactc agacttgcca
4681 ggtacatggt ctgttttctg tatagtctac agtctagaca tttagtgttt atgtctgcct
4741 tccaaggtta ttttgaccag gggtatcaaa agtcactgag caccattgtt tcccatgtta
4801 tgccaggctt ggttggctag gggctatgtt aaaggcttta tatgagccct tccaggcagg
4861 agcttgaagg tccatttaat ttaaggtcac aggtggctgt tgcatcacag aactggaaat
4921 tgagggctta acttcacaga aaaatccatg gttgagacaa tttaatgtct aatgacatgg
4981 agagtaaaag tgatcctctg ggcaaactaa gcatggagtc ataatattat gaagagcatt
5041 agaagcaaca ttaggaacag aatatgccag ctggaaatac aggcttgatc aacttctgaa
5101 agatccattt ctatctaaag taaatacatg agaaggtcat tatacccaag tgaatgtgaa
5161 ggcctacact gccttccgtc tgaatctttt gcaaacctaa catctaaagc ttgactgaca
5221 agttcatatt catctacttc tattttccta ggacattgaa tttaggttaa gcagtaatag
5281 atcaagaaga gggagtccag gatttgctta ccagtataaa tatatgtggt atctaaactg
5341 ggaagcagtt caattagttt taggtgaggc attcatgttg tatgtgtgca tatgtatgag
5401 tcaaatccag ttaggtctta gaatcagaat acatagtgta gacactatta tgtagctcat
5461 atatagcaga atatgtcata tttggctaac ccaagtgggc atgctatgag gactaacagg
5521 gcagataatg ttgtgacatc acaaactata cattgcattt ctgtgggtct cagctagcca
5581 tcagctatta ggttttaata ccatgaaagt aaaggttatg gggttgtttc ttgtttgttt
5641 gatttgtttt gaacttttct ctcactactg cttctctggg aaaaacagat tttgggagaa
5701 tgaatcagtt aactgaaagt aggtttatta atactcttgt accagcttat ctctcaatta
5761 gcaatgggtc ttacagtaaa tatctgagtt tctactttgc tgcactgaaa tactgtgcct
5821 ttattataga actttgaaag ggtttcccat gagctggatg gtgggagcca cactatatgt
5881 gccatgctgg acatcaggcc agtactgcaa tgcagtggtg tatttgatgt ctttcaggtg
5941 acttcatggt catgacattc ttcttcaatg taagcaggag gtttggcttc attgtctttc
6001 aaaactatat cccttcatct gttaccacaa tgctttcctg ggtgtccttc tggatcaaga
6061 tagaagctgc tgctgccagg gcctctgtag gtaagaaagt atggtgatct taaatgtgat
6121 catatgtcat agattaacat tgccttctcc tgttgtcctg cagcactgtc aggagcttag
6181 cccaccttca ctccttgctc ttataggggt cagttctgtg ctcaccatgg ccacactggg
6241 taccttttct cgtaagaatt tccctcgtgt ctcctatctc acagctttgg acttctatat
6301 tgcaatttgt ttcgtcttgt gcttctgtac tctactagag ttcactgtgc tcaacttcct
6361 gacctacaat aatattgaac gacaggcttc tccaaagttc taccaagtaa gaaccacgtg
6421 ttggtatggg aagcaaaact ttagactgaa gataggaggg ttatggcact tgtgtgacta
6481 cctttccaag tgatgagaat ttccctgggg ttatagagga aataaacttg ctgtgatatc
6541 caggaaggcc tagaactgat gtggagagtg tagtttctag gaaattctag gcaacttttc
6601 ttcttgactc actttccctt gaccattttg ttatctttat ttttctattt cagtttccaa
6661 ccaatagccg tgctaatgca cgtactcgtg ctcgtgcccg cactcgtgct cgtgctcgtg
6721 cccgtgctcg tcagcagcag gaagtgtttg tgtgtgagat tgttacctat gaggaaaatg
6781 ctgaagaggg ttaccagtgg tctccaagat caagaagacc tcagtgtccc tggaggcgat
6841 gtggccgaag ctatgtgtgc ttcagggttc tcaggaagta tttctgcatg gttcctggtt
6901 gtgagggcaa cagctggcag cggggccgca tctgcatcca cgtttatcgc ctggataact
6961 actcgcgggt gcttttcccc attacattct tcttctttaa tgtggtctac tgggtgattt
7021 gccttaacct gtaggctcca gctggtagct catggggcaa tcacctcagt tccccaggag
7081 gtcctaagcc cctttgtcaa gggagttggg agacaatagc aacagcagca agcctgagga
7141 gagtttgtct ttgctgctcc tccttttgtt ggcccccttca ctcaatcttt taaacagcac
7201 ttctcaagta acagcccacc tctctattct tcaaagagta tccatgatgt tcagtgtgcc
7261 cacaattgag cagataagct atctcttggt tgtgtttgca gttactgttt ttccccagga
7321 ggtcatggta ccatttgtgg tgctaagggg cccagctcaa gctcagccct agaatgcaca
7381 gagcaacaac agtatagcag aaggaaggtc ctcatcctta agtctttaag tcaggctatt
7441 tgatttttc tccctgctct ctcttcctct acacacaca
//
```

Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = U92284 | |
|---|---|
| *gi* | *Update Date* |
| 2455328 | 01/01/98 |

***This sequence was released by NCBI on 01/01/98***

Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez ?

Other Formats: FASTA Graphic

Links: Related Sequences

```
LOCUS       HSU92285     6146 bp    mRNA            PRI       04-FEB-1998
DEFINITION  Human GABA-A receptor epsilon subunit (GABRE) RNA, alternative
            transcript.
ACCESSION   U92285
NID         g2735330
KEYWORDS    .
SOURCE      human.
  ORGANISM  [illegible]
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Alternative transcripts of a gene encoding the GABA-A receptor
            epsilon subunit on chromosome Xq28
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6146)
  AUTHORS   Hanna,M.C., Hales,T.G. and Kirkness,E.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1997) Department of Molecular and Cellular
            Biology, The Institute for Genomic Research, 9712 Medical Center
            Drive, Rockville, MD 20850, USA
FEATURES             Location/Qualifiers
     source          1..6146
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
     misc_RNA        1..6146
                     /gene="GABRE"
                     /note="RNA transcript is initiated from within the GABRE
                     gene, and therefore contains intron sequence with respect
                     to the subunit transcript"
     misc_feature    1..3863
                     /gene="GABRE"
                     /note="intron 6 of GABRE; GABRE gene sequence deposited in
                     GenBank Accession Number U92283"
     gene            1..6146
                     /gene="GABRE"
     stem_loop       12..96
                     /gene="GABRE"
     stem_loop       1065..1147
                     /gene="GABRE"
     misc_feature    3864..6146
                     /gene="GABRE"
                     /note="exons 7, 8 and 9 of GABRE; GABRE gene sequence
                     deposited in GenBank Accession Number U92283"
BASE COUNT     1440 a   1519 c   1458 g   1729 t
ORIGIN
        1 gtcttataat tgctaagcac ttacaactgt ttgcagagga aactgagact ttgtaactat
       61 gtctcagtct catctgcaaa gaagtaagtg ctttgccaag ctccttgaga ggttaggtaa
      121 gtagataaag ttctgctgct gtcggaatgt gcagctggct ttttcatgca gacccttcag
      181 tttcgaggtt acaactctga cctctttgga tgactttggg gaatggagct cgtgtgagtt
      241 ctccataccc agaaccaatc cagtctggtt gaatgggaag caaagtccat tgtagtggga
      301 ggtggaggct agagttctaa tgtcagctag tttaaggctg ggaaagtctg gaggaagtta
      361 cagcagctac actggctgct gcattgacat ttatcttaaa ggaacaagtc tgaaaagcac
      421 agattcttat caaaggcttc atggtggatt ccacatagac atagtggcca ctggttttct
      481 gacctttttct ctgacaaaga ctaaagggga aggtcctggg tatcttacac ttcagctccc
      541 aattagatgt gagcaccttc acttatgttc ctaggtgacc tgaatgagga gccaagggac
      601 ctccccaggg tagctcccag agcaaccctg gaaacactct tcacacatcc tgaccaagtt
      661 cagggcagtg aaggcactgc cctcatcgtt tccagaatgt ggatggagcc agtcacccaa
      721 ccagccattt gtcgtgagag gcatcttgtt ctgctaccat gtgactaggc agaaaatctg
      781 cttttgtttc atttattgag tcagtctctg gatgagggaa agctcatgct catgtggcta
```

```
 841 gagctttgct tgcacagtat taggcagggg cagagggctg ggctaccttа aaaatacttg
 901 ccctttttct tggggactct ggggaagcgg ttttactacc tttgacttgg gagccttgct
 961 cttctgccag ctaaccatgg gcctgcctct tggttttctg cacctcagct tttcccggat
1021 aggtggggac ccatcatcaa aagtgacaga gaagataagg cccaggggct ttcaagtcac
1081 tagtggttcc gtttagtaga tgattgtgca ttgtttcaaa atggtgccct agtgactaca
1141 aagccccaga gccagcatca tcatcaaagc aatgacagta ggtaagcacc agacctcctt
1201 gggagtgagg aggattcttg aggagaaaag aggtcttctt tctcctctgc tggagactag
1261 ttgatctgga gacgtggttc cttcaatgtc agagttatct ttgggactgg tctcaaactc
1321 ttccagttgg gccctggggc aggtctctcc atctggagca tacttacgtg ctcggcgatt
1381 aagggttcag aatgcagtgg tagcctgcta ctctggccat cttggacctt gatccagaga
1441 atctctgctt caggagcttc taagagagtc cagccctgcc tccagagaga ggcttgccct
1501 tcactgatgg ctgtggagcc tctgatggaa tattattgct ggtcaggaat tcactgtctt
1561 acaaggaggt ttccttcttc tctagacagt tctgttcatc aaaaaactct ccctgttctt
1621 ctgaaattgg agtctctgga agttccacac attaagctta gttctttttc cttggaactg
1681 tccaggttac attagtccag ccactgtttc acaggaccga gattaaacga tcaacatcat
1741 cattcccggc atggatcata gtctgttgta gtctacatag ccctagttta tttttcttcc
1801 cttattcttc aaagctttgg gtccattcat tcttctagtc ccagtcctct ggacatggtc
1861 tatttaattg tgtccctctg acactgcagt gaccaaccat gatctggtca aagaggataa
1921 gagtttgagc agaaaaccat ctttagcata tatttttttg ctttggttca tcagccccag
1981 atatattgtt ttccttaccc gtgcttctct cactcctcaa gaagaagaaa gtgtgtgtta
2041 gcatctttct cttgtccttc aagacaaatt ggcatctctt gacgagcgga gaaggttctt
2101 ttttggccag aataaataaa attaaaatag aatcatccaa cagaataata aatcttcgtg
2161 caacaagaat atattatata aacccagcaa ttttgcaggg cctgggtata actaattaga
2221 agtgtcttaa attgcagtca agatcccacg gcaagaggac ttttgataaa tacattctgg
2281 ccagtaggca agtgcgaggg tggtccgtgc agcagctctg gaggagttct atcccaaagc
2341 tatactcaac acacaggttt cccactgaca acaggtcgct cccttgcctt cttccagaag
2401 aatctgagaa gctttgctcc ttgagtttca gtgctgccaa ggtgagtacg aaaggctgct
2461 cttctcattc agctccagcc cacccagacc tgctgggcag ttgatccact ttccaaaata
2521 ggaggacaca cggacaggtt agtgttctgg tctgctttac aaagctgttg cctgacagga
2581 gcaagagttg ctgagtgtct gctgggttcc aggctgttct gagcttggat gggcaggggc
2641 taagccacag ggcctgcatg agccctgcct tgaagggact taaaagacga cctaattata
2701 ggcctaggaa ttttacagta ttgcaactgc aatgtgatgc tgaaagtgga aaatgatgtc
2761 ctgggctcag agaaaagccc acaccagcct gggagtcatg atagcagcag agtgcttggg
2821 gagggtgtgt cagagcataa agcagcatga atgctacaaa agaagatgcc aactagagat
2881 ataggttgtc atcaggtccc ggaggagcca tgaccgtcta gctgagagcc atgaccaagg
2941 acacaatgtc caagtgactg tgaggacctc agtctgccct gtggatgtgt atgccacaga
3001 cctgacttct ggagggctga ctgaaatgtt cattttaagc tttttcttct ctttccctga
3061 aacactcagt ttgggttagg ggtcatagac taagaccaaa gagtccaggg ttagaatctt
3121 ggtgtaaaat tgcaggccat ctcaggaaat ctgtgagcag atgggattgg ctttgggtaa
3181 ggtgcgtgtg gaaaatgtca gtgggagccg ggtcatggtg ggcctttagc atcagattcc
3241 agagtgcaga tagtctgtat agctcatgtg aaacagggag ccaccaaaac tttggggagc
3301 aggctagtgc cggttttgac cacctgtgga gcagtgctca ctcacgaagg cattttgcca
3361 tcacatgaat gtgcagaaag gaggccaaaa gcattctgtg cttctccacc acagcacaga
3421 cttccctagt ctcatttgct gagagtagac attctgaggg ccagcagtgc aggtgtgatg
3481 tgcctcagag ggtatgaagc ccttagtcag ccatctggat atcagctgcg tgggcatgat
3541 atctagaagg ctaattgatt ttttcacttt cacctgactc tcttgccaac ctgcagagac
3601 agacattggg tgtaggacag tgaactgaga aggaagctat taagattctg gccttggctt
3661 agctctcaac tggccattgg tcttgcagta agtctttttt ctgggcttct tctggtccta
3721 tttgtatgta ttgcattgtc acatcatgcc tctatcctag ggaatactgt gagctgaaaa
3781 atgagaccct tactgttcac gtcctgctaa gggggaccgt cgtgtcagca ctgtaatgca
3841 gtgatgtttt ttgtgtcttt caggtgactt catggtcatg acgattttct tcaatgtgag
3901 caggcggttt ggctatgttg cctttcaaaa ctatgtccct tcttccgtga ccacgatgct
3961 ctcctgggtt tccttttgga tcaagacaga gtctgctcca gcccggacct ctctagggat
4021 cacctctgtt ctgaccatga ccacgttggg caccttttct cgtaagaatt tcccgcgtgt
4081 ctcctatatc acagccttgg atttctatat cgccatctgc ttcgtcttct gcttctgcgc
4141 tctgttggag tttgctgtgc tcaacttcct gatctacaac cagacaaaag cccatgcttc
4201 tcctaaactc cgccatcctc gtatcaatag ccgtgcccat gcccgtaccc gtgcacgttc
4261 ccgagcctgt gcccgccaac atcaggaagc ttttgtgtgc cagattgtca ccactgaggg
4321 aagtgatgga gaggagcgcc cgtcttgctc agcccagcag ccccctagcc caggtagccc
4381 tgagggtccc cgcagcctct gctccaagct ggcctgctgt gagtggtgca agcgttttaa
4441 gaagtacttc tgcatggtcc ccgattgtga gggcagtacc tggcagcagg gccgcctctg
4501 catccatgtc taccgcctgg ataactactc gagagttgtt ttcccagtga ctttcttctt
4561 cttcaatgtg ctctactggc ttgtttgcct taacttgtag gtaccagctg gtaccctgtg
4621 gggcaacctc tccagttccc caggaggtcc aagccccttg ccaagggagt tgggggaaag
4681 cagcagcagc agcaggagcg actagagttt ttcctgcccc attccccaaa cagaagcttg
4741 cagagggttt gtctttgctg cccctctccc ctacctggcc cattcactga gtcttctcag
4801 cagaccattt caaattatta ataaatgggc cacctccctc ttcttcaagg agcatccgtg
4861 atgctcagtg ttcaaaacca cagccactta gtgatcagct ccctaaaacc atgcctaagt
4921 acaggcggat tagctatctt ccaacaatgc tgaccaccag acaattactg catttttcca
4981 gaagcccact attgcctttg tagtgctttc ggcccagttc tggcctcagc ctcaaagtgc
5041 accgactagt tgcttgccta tacctggcac ctcattaaga tgctgggcag cagtataaca
```

```
     5101 ggaggaagag atccctctcc tttggtcaga ttattatgtt ctcagttctc tctccctgct
     5161 acccctttct ctgcagatag atagacactg gcattatccc tttaggaaga gggggggca
     5221 gcaagagagc ctatttggga cagcattcct ctctctctgc tgctgtgaca tctccctctc
     5281 cttgctggct ccatctttcg tctgcactac caattcaatg cccttcatcc aatgggtatc
     5341 tatttttgtg tgtgattata gtaactactc cctgctttat atgccaccct cttccttctc
     5401 tttgacccct gtgactcttt ctgtaacttt cccagtgact tcccctagcc ctgacccagg
     5461 cactaggcct tggtgacttc ctggggccaa gaaactaagg aaactcggct ttgcaacagg
     5521 cattactcgc cattgattgg tgcccaccca gggcacactg tcggagttct atcacttgct
     5581 tgacccctgg acccataaac cagtccactg ttatacccgg ggcactctaa ccatcacaat
     5641 caatcaatca aattccctta aatttgtatg gcactggaac tttggcaaag cacttttgac
     5701 aagttgtgtc tgattggagc ttcatgatag ccttgtgaca tctttagggc aggattctta
     5761 tccccatttt gcagatgaaa accctgagtc acagatttct gtgggactgt ggatctcact
     5821 ggaagctatc caagagccca ctgtcacctt ctagaccaca tgatagggct agacagctca
     5881 gttcaccatg attctcttct gtcacctctg ctggcacacc agtggcaagg cccagaatgg
     5941 cgacctctct ttagctcaat ttctgggcct gaggtgctca gactgccccc aagatcaaat
     6001 ctctcctggc tgtagtaacc cagtggaatg aatttggaca tgccccaatg cttctatatg
     6061 ctaagtgaaa tctgtgtctg taatttgttg gggggtggat agggtggggt ctccatctac
     6121 tttttgtcac catcatctga aatggg
//
```

Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = U92285 | |
|---|---|
| *gi* | *Update Date* |
| 2755330 | 02/05/98 |

***This sequence was released by NCBI on 01/01/98***

Disclaimer

NCBI Entrez Nucleotide QUERY BLAST Entrez2 ?

**Other Formats:** FASTA | Graphic

**Links:** MEDLINE | Related Sequences

```
LOCUS       HSY09764    10897 bp    DNA                 PRI       31-OCT-1997
DEFINITION  Homo sapiens GABRE gene, exon 2-8.
ACCESSION   Y09764
NID         g2285959
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10897)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 10897)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1..10897
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="q28"
                     /clone="cosmid Qc11C8"
     gene            1334..10897
                     /gene="GABRE"
     exon            1334..1551
                     /gene="GABRE"
                     /number=2
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            2000..2288
                     /gene="GABRE"
                     /number=3
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            3346..3428
                     /gene="GABRE"
                     /number=4
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            4736..4873
                     /gene="GABRE"
                     /number=5
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8163..8315
                     /gene="GABRE"
                     /number=6
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8456..8655
                     /gene="GABRE"
                     /number=7
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
     exon            8939..10897
```

```
                     /gene="GABRE"
                     /number=8
                     /usedin=Y09763:gab_mrna
                     /usedin=Y09763:gab_cds
BASE COUNT     2630 a    2703 c    2465 g    3099 t
ORIGIN
        1 gcttttaaaa agacttttaa ttatattttt taaagacata taaaggtagg ggaacagtgc
       61 acccccattg tttgtgaact catggccact cttatttttct tttacaccac ccaccctcca
      121 attccaactt agattgtctt gaagcatatc tcagacatca tatcatttta tatgtaattg
      181 ttttagtatg tatttctagt cattaatatt tcacaaacat aagaaaatac cataattaca
      241 ccaaaaatta aagaataatt tattcatgtc tcaactgtcc actcagtgtt caaatctctc
      301 ctattgtgtc ataaatgatt tctgtttgtt tttcaagagt ttgcttttaa ataaaataag
      361 atccagatat tagcaagtgg ggcattttga tttttaaaaa cacttttttat ggaattagaa
      421 catgtataca gagaagtgct caaatcataa gtgtacagct gatgagttgt caaaaaatga
      481 ccacagcggt gtaaagaaag ccaaatcaag gacccgaatg tgagcaggac ctcagaagcc
      541 ccctttgtca ctgcctccca gcaaaggcag cactatccgg acttctaaca ccatcggtga
      601 gtttcatacc ttggcagatg gcctttaaca tttttgttta attcaattat tcttactaat
      661 cttcttcttt ttcttggctg tggtgcatgg ctgtggagct cagggtggac tcctgttggg
      721 cagccagttc ctggatggct gtctgtgggt ggaggactcc tgcctttcct gtttagacac
      781 ccacaaaggc tgctctttag cctccttccc ttcatcccct tcccctgccc ccagtgcaac
      841 gagtattaca caaccaacaa aaccgcaaaa tattcccaca attttctggt cctctctggg
      901 agaggccgct ctggcttttc ctctcagccc tggccctctg cctgctcctc actcctggtt
      961 ggtgctggtc aggctgacta gaggccaagg cgaccaacac taggcaaacg cggccagcgc
     1021 tcagacataa atgccctctt catttcacgt gtaacattct tttaaaatct aggtcttggt
     1081 tttgttgatt ttttcttaaa taaaagagtg atcataaaag agggacagca tagaaagtcc
     1141 ccaaagagca gcaaggtttt aaagaaattc acaagcctaa tctgtcactg tcttataatt
     1201 tgctattacc agtcacaatt taactaggtt ttgtgttgaa aacttgtttt ggtttgcttc
     1261 tgtcccaaga ggcactagct ggggccccta cagagtgcag ggcagagctt catttttcgt
     1321 ttgaatgttc tagggtcgag ggacctcaga ctgaatcaaa gaatgaagcc tcttcccgtg
     1381 atgttgtcta tggcccccag ccccagcctc tggaaaatca gctcctctct gaggaaacaa
     1441 agtcaactga gactgagact gggagcagag ttggcaaact gccagaagcc tctcgcatcc
     1501 tgaacactat cctgagtaat tatgaccaca aactgcgccc tggcattgga ggtgaggagc
     1561 agaacgacgt tcttcccctc ctagagggtc caggggttga gggcataggc atggagaatg
     1621 cacctgggca gtaacagagg gtgccatgct catggacagg aacatctgct attgacctgt
     1681 caggtaagag atattaactc tattctcagc agtgtcattg accttgatca agacttttcc
     1741 cttctctcgc cctcagtttt tccagtggta aaatgagagg actaaactag attgttgatc
     1801 ttcaagatgt gtgtccaatt cttaacagtc cgtgagcttg gttttgccat gaaagaataa
     1861 ataaagaaat aggattagat gctgaaactg tgtggtccaa cacttacttg actccccttt
     1921 catcccctct gaccacttcc tcccccgtcc catgcgcctg tgtgacactt accctctgct
     1981 ccgcccccctg ccattagaga gaagcccact gtggtcactg ttgagatctc cgtcaacagc
     2041 cttggtcctc tctctatcct agacatggaa tacaccattg acatcatctt ctcccagacc
     2101 tggtacgacg aacgcctctg ttacaacgac acctttgagt ctcttgttct gaatggcaat
     2161 gtggtgagcc agctatggat cccggacacc ttttttagga attctaagag gacccacgag
     2221 catgagatca ccatgcccaa ccagatggtc cgcatctaca aggatggcaa ggtgttgtac
     2281 acaattaggt atgtcaagcc tctggagtct cacttcctgg aattctctct ccccttctga
     2341 taatttagc taaagatcca tgggcagaga tctcatcctg aatgatacct ctaagggcct
     2401 gtccagcttt cctagaccat gagctcagcc cccttatgta acagatatag aggcctcaaa
     2461 atagaaagat attgcttaaa gccacacacc aagtttgtgg cagagctgga actggtactc
     2521 agttacttgg ctccgagtcc agagctccct caactaggat gtgccagtat gactgcatta
     2581 tctagacaat tccatcctaa gtgggcactc gatacaaaga tacgtccaca gtggtggaat
     2641 tgttcaggca gagcagcagc acggtagtgg caaaggtacc taagatcgag ttggatactt
     2701 gaattcccag caggggaagg ttgtgtgtgg gggatagcag ggaggatgtt ggcaggtcct
     2761 ggaaactagg ctgggcgaga aaacaaaagc cgatcgaagt tgctccatac gtttctctaa
     2821 tgatggagcc caaagtaacc agatacttct aagctgtttg tttgttttgt tttgttttgt
     2881 tttgttttgt tttgttttgt tttctctctt gttatctctc ctttgagctt tttgtcttaa
     2941 attctagcga ggtccaggca cggtggctca cgcctgtgat cccagcactt tgtgaggctg
     3001 aggcaggcag atcacttgag gtcaggagtt cgagaccagc ctggccatca tgggaaaacc
     3061 ctgtctccac taaaaatgca aaaattagca gggtgtgctg gcactaattc cagctactcg
     3121 ggaggctagg gcatgagaat tgcttgagcc tgggaggcaa gaggctgcag tgagctgacg
     3181 tcacgccact gccctccagc ctgggtgaca gagtgagact ctgtctcaaa caaacaaaga
     3241 aaaaaattga ctctggccat tcattggtgg tagtccctag accaaagctg ggtggatacg
     3301 gaagtgctta gggccagcct gatgaggctc ctttctccct tccaggatga ccattgatgc
     3361 cggatgctca ctccacatgc tcagatttcc aatggattct cactcttgcc ctctatcttt
     3421 ctctagctgt gagtaccttc ttaagtttct ggggccccag aaacatgctg ggctccttct
     3481 ttttctcatc cttgccattt acatttttct gcctctgctt ttcttctaaa atgctgccaa
     3541 ggttgtgcag gacttccatc ctccaccctc atttcctttc ctgccaacaa tactgtgttg
     3601 ctcatccctt ccacgtgcct ctgaagcgta tctcaagtat gtctgctcct ctccatctcc
     3661 actggcacta ccttggttta ggcctttgtt atcttccacc tggacttttg ccacatcttc
     3721 actttgaaac tgcacatgtc caaaatgaaa ttcattgtct cctccaaacc tctaccacca
```

```
3781 aaacaagtgt gttgcttctg ggttcccatc tgtctcagtg aagaggacca tcactcaccc
3841 agctgcgcaa atcaagaact ttgatgttcc ctctccctca cctcctgcat ctaatcaatc
3901 agcacatcct gttggtgttt cctcccagtc tctatcgatg ctgtctattt ctctgcaccc
3961 tgtacagctt tgacttccac ctgcgttaat ttaattctgc ctggattact acactggcct
4021 ccttgacaac atgttgtcct cacagaagga ccaaagtgac ctacctgaag ggtcacctag
4081 gttgggtcac ttcttagtct cgaatctgcc gttaactctc atggatcaat ttgaaattcc
4141 ttagaatgaa cctcaaggcc attcatgaac tggaccctgc cacccaatcc tgtgcacctc
4201 atcctctgtg agctagccat cctgaacttt tgtcctttcc acaatacacc aggtgtttca
4261 cctttctata ctgcccctta acccccttcaa cctcattctt attgagaata tttacttgag
4321 tttcaagatt taatgggaat atcacctgct ttatgaagtc ttttttgagt atgtccccaa
4381 gtgaccttta tctactttgt ttcccccgct gttctgtgga cttaggtttt tcagagctcc
4441 tccaaaaatc acagtagtat actcactgtc ttataaaatt aaatgtgatt gcttgagggt
4501 agggttcatg ccttgctcat ctctgtattt ctggcctagg gcctgatact gaggaatgct
4561 cagtaaacgc actcattgaa tggacttcaa caatgaggta agagaggcaa ggtcccacag
4621 ctggtgaggc cagagacagg actccaaggc attgtgcagg ctgacttcat gctattggag
4681 acctcaggtg ggcttccaag tctcataaga ccctctttct cacattcctt tccagtttcc
4741 tatcctgaga atgagatgat ctacaagtgg gaaaatttca agcttgaaat caatgagaag
4801 aactcctgga agctcttcca gttggatttt acaggagtga gcaacaaaac tgaaataatc
4861 acaaccccag ttggtgacct gaatgaggag ccaagggacc tccccagggt agctcccaga
4921 gcaaccctgg aaacactctt cacacatcct gaccaagttc agggcagtga aggcactgcc
4981 ctcatcgttt ccagaatgtg gatggagcca gtcacccaac cagccatttg tcgtgagagg
5041 catcttgttc tgctaccatg tgactaggca gaaaatctgc ttttgtttca tttattgagt
5101 cagtctctgg atgagggaaa gctcatgctc atgtggctag agctttgctt gcacagtatt
5161 aggcaggggc agagggctgg gctacctaaa aaatacttgc ccttttttctt ggggactctg
5221 gggaagcggt tttactacct ttgacttggg agccttgctc ttctgccagc taaccatggg
5281 cctgcctctt ggttttctgc acctcagctt ttcccggata ggtggggacc catcatcaaa
5341 agtgacagag aagataaggc ccaggggctt tcaagtcact agtggttccg tttagtagat
5401 gattgtgcat tgtttcaaaa tggtgcccta gtgactacaa agccccagag ccagcatcat
5461 catcaaagca atgacagtag gtaagcacca gacctccttg ggagtgagga ggattcttga
5521 ggagaaaaga ggtcttcttt ctcctctgct ggagactagt tgatctggag acgtggttcc
5581 ttcaatgtca gagttatctt tgggactggt ctcaaactct tccagttggg ccctgggca
5641 ggtctctcca tctggagcat acttacgtgc tcggcgatta agggttcaga atgcagtggt
5701 agcctgctac tctggccatc ttggaccttg atccagagaa tctctgcttc aggagcttct
5761 aagagagtcc agccctgcct ccagagagag gcttgccctt cactgatggc tgtggagcct
5821 ctgatggaat attattgctg gtcaggaatt cactgtctta caaggaggtt tccttcttct
5881 ctagacagtt ctgttcatca aaaaactctc cctgttcttc tgaaattgga gtctctggaa
5941 gttccacaca ttaagcttag ttctttttcc ttggaactgt ccaggttaca ttagtccagc
6001 cactgtttca caggaccgag attaaacgat caacatcatc attcccggca tggatcatag
6061 tctgttgtag tctacatagc cctagtttat ttttcttccc ttattcttca aaggtggggg
6121 tccattcatt cttctagtcc cagtcctctg gacatggtct atttaattgt gtccctctga
6181 cactgcaatg accaaccatg atctggtcaa agaggataag agtttgagca gaaaaccatc
6241 tttagcatat attttttttgc tttggttcat cagccccaga tatattgttt tccttacccg
6301 tgcttctctc actcctcaag aagaagaaag tgtgtgttag catctttctc ttgtccttca
6361 agacaaattg gcatctcttg acgagcggag aaggttcttt tttggccaga ataaataaaa
6421 ttaaaataga atcatccaac agaataataa atcttcgtgc aacaagaata tattatataa
6481 acccagcaat tttgcagggc ctgggtataa ctaattagaa gtgtcttaaa ttgcagtcaa
6541 gatcccacgg caagaggact tttgataaat acattctggc cagtaggcaa gtgcgagggt
6601 ggtccgtgca gcagctctgg aggagttcta tcccaaagct atactcaaca cacaggtttc
6661 ccactgacaa caggtcgctc ccttgccttc ttccagaaga atctgagaag ctttgctcct
6721 tgagtttcag tgctgccaag gtgagtacga aaggctgctc ttctcattca gctccagccc
6781 acccagacct gctgggcagt tgatccactt tcccaaatag gaggacacac ggacaggtta
6841 gtgttctggt ctgctttaca aagctgttgc ctgacaggag caagagttgc tgagtgtctg
6901 ctgggttcca ggctgttctg agcttggatg ggcaggggct aagccacagg gcctgcatga
6961 gccctgcctt gaagggactt aaaagacgac ctaattatag gcctaggaat tttacagtat
7021 tgcaactgca atgtgatgct gaaagtggaa aatgatgtcc tgggctcaga gaaaagccca
7081 caccagcctg ggagtcatga tagcagcaga gtgcttgggg agggtgtgtc agagcataaa
7141 gcagcatgaa tgctacaaaa gaagatgcca actagagata taggttgtca tcaggtcccg
7201 gaggagccat gaccgtctag ctgagagcca tgaccaagga cacaatgtcc aagtgactgt
7261 gaggacctca gtctgccctg tggatgtgta tgccacagac ctgacttctg gagggctgac
7321 tgaaatgttc attttaagct ttttcttctc tttccctgaa acactcagtt tgggttaggg
7381 gtcatagact aagaccaaag agtccagggt tagaatcttg gtgtaaaatt gcaggccatc
7441 tcaggaaatc tgtgagcaga tgggaatggc tttgggtaag gtgcgtgtgg aaaatgtcag
7501 tgggagccgg gtcatggtgg gcctttagca tcagattcca gaatgcagat agtctgtata
7561 gctcatgtga aacagggagc caccaaaact ttggggagca ggctagtgcc ggtcttgacc
7621 acctgtggag cagtgctcac tcacgaaggc attttggcat cacatgaatg tgcagaaagg
7681 aggccaaaag cattctgtgc ttctccacca cagcacagac ttccctagtc tcatttgctg
7741 agagtagaca ttctgagggc cagcagtgca ggtgtgatgt gcctcagagg gtatgaagcc
7801 cttagtcagc catctggata tcagctgcgt gggcatgata tctagaaggc taattgattt
7861 tttcactttc acctgactct cttgccaacc tgcagagaca gacattgggt gtaggacagt
```

```
   7921 gaactgagaa ggaagctatt aagattctgg ccttggctta gctctcaact ggccattggt
   7981 cttgcagtaa gtctttttc tgggcttctt ctggtcctat ttgtatgtat tgcattgtca
   8041 catcatgcct ctatcctagg gaatactgtg agctgaaaaa tgagaccctt actgttcacg
   8101 tcctgctaag ggggaccgtc gtgtcagcac tgtaatgcag tgatgttttt tgtgtctttc
   8161 aggtgacttc atggtcatga cgattttctt caatgtgagc aggcggtttg gctatgttgc
   8221 ctttcaaaac tatgtccctt cttccgtgac cacgatgctc tcctgggttt ccttttggat
   8281 caagacagag tctgctccag cccggacctc tctaggtaag aggagaaaca ggtatacgca
   8341 taggcacatg gctgggagtt ggctgggcca gggcagagtt gccttgtcat ggagtctttt
   8401 aaccaatgtc gcacataggt caggagctga gcccatcact cttgtgctct tgcagggatc
   8461 acctctgttc tgaccatgac cacgttgggc acctttttctc gtaagaattt cccgcgtgtc
   8521 tcctatatca cagccttgga tttctatatc gccatctgct tcgtcttctg cttctgcgct
   8581 ctgttggagt ttgctgtgct caacttcctg atctacaacc agacaaaagc ccatgcttct
   8641 cctaaactcc gccatgtatg agctgggtat gggagtggtg gcaaggcttt ggagtgtaga
   8701 gacatgctag caagggtact ggggatatgg cacatgggtg gtcagcttgc tgagtgatgg
   8761 aatgttaccc agggtggtgg cggggttgaa tcaacttcct gatgtaatgg tgagaagttg
   8821 gaggagagaa gccaagatat ggtgtgccaa agacagtttc cagaaaatcc ggaggcagca
   8881 cttagacttg ggttatcttc ccttgacttt tccccacttc tttccttgtc cattttagcc
   8941 tcgtatcaat agccgtgccc atgcccgtac ccgtgcacgt tcccgagcct gtgcccgcca
   9001 acatcaggaa gcttttgtgt gccagattgt caccactgag ggaagtgatg gagaggagcg
   9061 cccgtcttgc tcagcccagc agccccctag cccaggtagc cctgagggtc cccgcagcct
   9121 ctgctccaag ctggcctgct gtgagtggtg caagcgtttt aagaagtact tctgcatggt
   9181 ccccgattgt gagggcagta cctggcagca ggcccgcctc tgcatccatg tctaccgcct
   9241 ggataactac tcgagagttg ttttcccagt gactttcttc ttcttcaatg tgctctactg
   9301 gctttttgc cttaacttgt aggtaccagc tggtaccctg tggggcaacc tctccagttc
   9361 cccaggaggt ccaagcccct tgccaaggga gttgggggaa agcagcagca gcagcaggag
   9421 cgactagagt ttttcctgcc ccattcccca aacagaagct tgcagagggt ttgtctttgc
   9481 tgcccctctc ccctacctgg cccattcact gagttttctc agcagaccat ttcaaattat
   9541 taataaatgg gccacctccc tcttcttcaa ggagcatccg tgatgctcag tgttcaaaac
   9601 cacagccact tagtgatcag ctccctaaaa ccatgcctaa gtacaggcgg attagctatc
   9661 ttccaacaat gctgaccacc agacaattac tgcatttttc cagaagccca ctattgcctt
   9721 tgcagtgctt tcggcccagt tctggcctca gcctcaaagt gcaccgacta gttgcttgcc
   9781 tatacctggc acctcattaa gatgctgggc agcagtataa caggaggaag agatccctct
   9841 cctttggtca gattattatg ttctcagttc tctctccctg ctaccccttt ctctgcagat
   9901 agatagacac tggcattatc cctttaggaa gaggggggg cagcaagaga gcctatttgg
   9961 gacagcattc ctctctctct gctgctgtga catctccctc tccttgctgg ctccatcttt
  10021 cgtctgcact accaattcaa tgcccttcat ccaatgggta tctatttttg tgtgtgatta
  10081 tagtaactac tccctgcttt atatgccacc ctcttccttc tctttgaccc ctgtgactct
  10141 ttctgtaact ttcccagtga cttcccctag ccctgaccag gcactaggcc ttggtgactt
  10201 cctggggcca agaaactaag gaaactcggc tttgcaacag gcattactcg ccattgattg
  10261 gtgcccaccc agggcacact gtcggagttc tatcacttgc ttgacccctg gacccataaa
  10321 ccagtccact gttatacccg gggcactcta accatcacaa tcaatcaatc aaattccctt
  10381 aaatttgtat ggcactggaa ctttggcaaa gcacttttga caagttgtgt ctgattggag
  10441 cttcatgata gccttgtgac atctttaggg caggattctt atccccattt tgcagatgaa
  10501 aaccctgagt cacagatttc tgtgggactg tggatctcac tggaagctat ccaagagccc
  10561 actgtcacct tctagaccac atgatagggc tagacagctc agttcaccat gattctcttc
  10621 tgtcacctct gctggcacac cagtggcaag gcccagaatg gcgacctctc tttagctcaa
  10681 tttctgggcc tgaggtgctc agactgcccc caagatcaaa tctctcctgg ctgtagtaac
  10741 ccagtggaat gaatttggac atgccccaat gcttctatat gctaagtgaa atctgtgtct
  10801 gtaatttgtt gggggtgga tagggtgggg tctccatcta ctttttgtca ccatcatctg
  10861 aaatggggaa atatgtaaat aaatatatca gcaaagc
//
```

Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = Y09764 | |
|---|---|
| ***gi*** | ***Update Date*** |
| 2285959 | 11/02/97 |

***This sequence was released by NCBI on 07/30/97***

*Disclaimer*

NCBI Entrez **Nucleotide QUERY** BLAST Entrez ?

**Other Formats:** FASTA | Graphic

**Links:** MEDLINE | Protein | Related Sequences

```
LOCUS       HSY09765     3150 bp    RNA             PRI       31-OCT-1997
DEFINITION  Homo sapiens mRNA for putative GABA receptor epsilon subunit.
ACCESSION   Y09765
NID         g2285960
KEYWORDS    GABA receptor; GABRE gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3150)
  AUTHORS   Wilke,K., Gaul,R., Klauck,S.M. and Poustka,A.
  TITLE     A gene in human chromosome band Xq28 (GABRE) defines a putative new
            subunit class of the GABAA neurotransmitter receptor
  JOURNAL   Genomics 45 (1), 1-10 (1997)
  MEDLINE   97480709
REFERENCE   2  (bases 1 to 3150)
  AUTHORS   Wilke,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1996) K. Wilke, Deutsches Krebsforschungszentrum,
            Abteilung Molekulare Genomanalyse (840), Im Neuenheimer Feld 280,
            D-69120 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1..3150
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /map="q28"
     CDS             55..1575
                     /note="putative"
                     /codon_start=1
                     /product="GABA receptor epsilon subunit"
                     /db_xref="PID:e1168937"
                     /db_xref="PID:g2285961"
                     /translation="MLSKVLPVLLGILLILQSRVEGPQTESKNEASSRDVVYGPQPQP
                     LENQLLSEETKSTETETGSRVGKLPEASRILNTILSNYDHKLRPGIGEKPTVVTVEIS
                     VNSLGPLSILDMEYTIDIIFSQTWYDERLCYNDTFESLVLNGNVVSQLWIPDTFFRNS
                     KRTHEHEITMPNQMVRIYKDGKVLYTIRMTIDAGCSLHMLRFPMDSHSCPLSFSSFSY
                     PENEMIYKWENFKLEINEKNSWKLFQFDFTGVSNKTEIITTPVGDFMVMTIFFNVSRR
                     FGYVAFQNYVPSSVTTMLSWVSFWIKTESAPARTSLGITSVLTMTTLGTFSRKNFPRV
                     SYITALDFYIAICFVFCFCALLEFAVLNFLIYNQTKAHASPKLRHPRINSRAHARTRA
                     RSRACARQHQEAFVCQIVTTEGSDGEERPSCSAQQPPSPGSPEGPRSLCSKLACCEWC
                     KRFKKYFCMVPDCEGSTWQQGRLCIHVYRLDNYSRVVFPVTFFFFNVLYWLVCLNL"
BASE COUNT      712 a    889 c    690 g    859 t
ORIGIN
        1 gccagagcgt gagccgcgac ctccgcgcag gtggtcgcgc cggtctccgc ggaaatgttg
       61 tccaaagttc ttccagtcct cctaggcatc ttattgatcc tccagtcgag ggtcgaggga
      121 cctcagactg aatcaaagaa tgaagcctct tcccgtgatg ttgtctatgg cccccagccc
      181 cagcctctgg aaaatcagct cctctctgag gaaacaaagt caactgagac tgagactggg
      241 agcagagttg gcaaactgcc agaagcctct cgcatcctga acactatcct gagtaattat
      301 gaccacaaac tgcgccctgg cattggagag aagcccactg tggtcactgt tgagatctcc
      361 gtcaacagcc ttggtcctct ctctatccta gacatggaat acaccattga catcatcttc
      421 tcccagacct ggtacgacga acgcctctgt tacaacgaca cctttgagtc tcttgttctg
      481 aatggcaatg tggtgagcca gctatggatc ccggacacct tttttaggaa ttctaagagg
      541 acccacgagc atgagatcac catgcccaac cagatggtcc gcatctacaa ggatggcaag
      601 gtgttgtaca caattaggat gaccattgat gccggatgct cactccacat gctcagattt
      661 ccaatggatt ctcactcttg ccctctatct ttctctagct tttcctatcc tgagaatgag
      721 atgatctaca agtgggaaaa tttcaagctt gaaatcaatg agaagaactc ctggaagctc
      781 ttccagtttg attttacagg agtgagcaac aaaactgaaa taatcacaac cccagttggt
      841 gacttcatgg tcatgacgat tttcttcaat gtgagcaggc ggtttggcta tgttgccttt
```

```
 901 caaaactatg tcccttcttc cgtgaccacg atgctctcct gggtttcctt ttggatcaag
 961 acagagtctg ctccagcccg gacctctcta gggatcacct ctgttctgac catgaccacg
1021 ttgggcacct tttctcgtaa gaatttcccg cgtgtctcct atatcacagc cttggatttc
1081 tatatcgcca tctgcttcgt cttctgcttc tgcgctctgt tggagtttgc tgtgctcaac
1141 ttcctgatct acaaccagac aaaagcccat gcttctccta aactccgcca tcctcgtatc
1201 aatagccgtg cccatgcccg tacccgtgca cgttcccgag cctgtgcccg ccaacatcag
1261 gaagcttttg tgtgccagat tgtcaccact gagggaagtg atggagagga gcgcccgtct
1321 tgctcagccc agcagccccc tagcccaggt agccctgagg gtccccgcag cctctgctcc
1381 aagctggcct gctgtgagtg gtgcaagcgt tttaagaagt acttctgcat ggtccccgat
1441 tgtgagggca gtacctggca gcagggccgc ctctgcatcc atgtctaccg cctggataac
1501 tactcgagag ttgttttccc agtgactttc ttcttcttca atgtgctcta ctggcttgtt
1561 tgccttaact tgtaggtacc agctggtacc ctgtggggca acctctccag ttccccagga
1621 ggtccaagcc ccttgccaag ggagttgggg gaaagcagca gcagcagcag gagcgactag
1681 agtttttcct gccccattcc ccaaacagaa gcttgcagag ggtttgtctt tgctgccct
1741 ctcccctacc tggcccattc actgagtttt ctcagcagac catttcaaat tattaataaa
1801 tgggccacct ccctcttctt caaggagcat ccgtgatgct cagtgttcaa aaccacagcc
1861 acttagtgat cagctcccta aaaccatgcc taagtacagg cggattagct atcttccaac
1921 aatgctgacc accagacaat tactgcattt ttccagaagc ccactattgc ctttgcagtg
1981 ctttcggccc agttctggcc tcagcctcaa agtgcaccga ctagttgctt gcctatacct
2041 ggcacctcat taagatgctg ggcagcagta taacaggagg aagagatccc tctcctttgg
2101 tcagattatt atgttctcag ttctctctcc ctgctacccc tttctctgca gatagataga
2161 cactggcatt atccctttag gaagaggggg gggcagcaag agagcctatt tgggacagca
2221 ttcctctctc tctgctgctg tgacatctcc ctctccttgc tggctccatc tttcgtctgc
2281 actaccaatt caatgccctt catccaatgg gtatctattt ttgtgtgtga ttatagtaac
2341 tactccctgc tttatatgcc accctcttcc ttctctttga cccctgtgac tctttctgta
2401 actttcccag tgacttcccc tagccctgac caggcactag gccttggtga cttcctgggg
2461 ccaagaaact aaggaaactc ggctttgcaa caggcattac tcgccattga ttggtgccca
2521 cccagggcac actgtcggag ttctatcact tgcttgaccc ctggacccat aaaccagtcc
2581 actgttatac ccggggcact ctaaccatca caatcaatca atcaaattcc cttaaatttg
2641 tatggcactg gaactttggc aaagcacttt tgacaagttg tgtctgattg gagcttcatg
2701 atagccttgt gacatcttta gggcaggatt cttatcccca ttttgcagat gaaaaccctg
2761 agtcacagat ttctgtggga ctgtggatct cactggaagc tatccaagag cccactgtca
2821 ccttctagac cacatgatag ggctagacag ctcagttcac catgattctc ttctgtcacc
2881 tctgctggca caccagtggc aaggcccaga atggcgacct ctctttagct caatttctgg
2941 gcctgaggtg ctcagactgc ccccaagatc aaatctctcc tggctgtagt aacccagtgg
3001 aatgaatttg gacatgcccc aatgcttcta tatgctaagt gaaatctgtg tctgtaattt
3061 gttggggggt ggatagggtg gggtctccat ctacttttg tcaccatcat ctgaaatggg
3121 gaaatatgta aataaatata tcagcaaagc
//
```

Save the above report in Macintosh Text format

NCBI **Sequence revision history** Entrez ?

| Revision History for Accession = Y09765 | |
|---|---|
| ***gi*** | ***Update Date*** |
| 2285960 | 11/02/97 |

***This sequence was released by NCBI on 07/30/97***
*Disclaimer*